

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

181	Db		TTCTGTTGGAGCCCGAGGATGTGTATCGTCAAGAACCAAGCCAGTGTGCTTGTGTGC	240
241	Qy		AAGCCCGTCCCGCCACGACAGTCTTTCAAAGTGCACACGGGAGTGGGTGCGCAGGTG	300
241	Db		AAGCCCGTCCCGCCACGACAGTCTTTCAAAGTGCACACGGGAGTGGGTGCGCAGGTG	300
301	Qy		GACCACTGTGATCGAGCGAGACACAGACGGGAGCAGTGGGTGCCCCACCATGGAGTCCGC	360
301	Db		GACCACTGTGATCGAGCGAGACACAGACGGGAGCAGTGGGTGCCCCACCATGGAGTCCGC	360
361	Qy		ATTAAATGTTCAAGGACAGAGTGCAGAGAGTGTTCGGGCTGGAGGAACTACTGGTGCCAG	420
361	Db		ATTAAATGTTCAAAGGACAGAGTGCAGAGAGTGTTCGGGCTGGAGGAACTACTGGTGCCAG	420
421	Qy		TGCGTGGCATGAGCTCTCTCGGGCACCAACCAAGAGTCAAGAGGCTTACATCCCGATAGCC	480
421	Db		TGCGTGGCATGAGCTCTCTCGGGCACCAACCAAGAGTCAAGAGGCTTACATCCCGATAGCC	480
481	Qy		AGATTGGCCAGAACTTCGAGCAGCAGCGCGTGGCCAAAGAGGTGTCTCTGGAGCAGGGC	540
481	Db		AGATTGGCCAGAACTTCGAGCAGCAGCGCGTGGCCAAAGAGGTGTCTCTGGAGCAGGGC	540
541	Qy		ATCGTGTGCCCTCGCGTCCACCGAGGGGATCCCTCCAGCCGAGGTGGAGTGTGCTCCGG	600
541	Db		ATCGTGTGCCCTCGCGTCCACCGAGGGGATCCCTCCAGCCGAGGTGGAGTGTGCTCCGG	600
601	Qy		AACGAGGACCTGTGTGACCCGTCCTCGAACCCCAATGTATACATCACCGGGAGCACAGC	660
601	Db		AACGAGGACCTGTGTGACCCGTCCTCGAACCCCAATGTATACATCACCGGGAGCACAGC	660
661	Qy		CTGTTGGTGCACAGGCCCGCTTTGTGACACGSCCAACTACACTTCGCTGGGCCAAGAAC	720
661	Db		CTGTTGGTGCACAGGCCCGCTTTGTGACACGSCCAACTACACTTCGCTGGGCCAAGAAC	720
721	Qy		ATCGTGCACTCGCCGACAGCGCTCCGCTGCTGTCTATCGTCTAGTGAAACGGTGGGTGG	780
721	Db		ATCGTGCACTCGCCGACAGCGCTCCGCTGCTGTCTATCGTCTAGTGAAACGGTGGGTGG	780
781	Qy		TCGACGTGGACCGAGTGGTCCGCTCGACGCGCAGCTGTGGCGCGGCTGGCAGAACCG	840
781	Db		TCGACGTGGACCGAGTGGTCCGCTCGACGCGCAGCTGTGGCGCGGCTGGCAGAACCG	840
841	Qy		AGCCGGAGCTGCACAAACCCCGCGCTCTCAAACGGGGCGCTTTTCTGTGAGGGGCGAAT	900
841	Db		AGCCGGAGCTGCACAAACCCCGCGCTCTCAAACGGGGCGCTTTTCTGTGAGGGGCGAAT	900
901	Qy		GTCAGAAACAGCTCGGCCACCCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
901	Db		GTCAGAAACAGCTCGGCCACCCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
961	Qy		AAGTGGTCCGCTGTGGGCTGGAATGCAACCACTGGCGGAGCCGTGAGTGTCTTGACCCA	1020
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1021	Qy		GCACCCGCAACGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
1021	Db		GCACCCGCAACGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
1081	Qy		AGTGACCTCTGTGTACACAGTGTTCGGCCCTGAGGACGTGGCCCTCATGTGGGGCTC	1140
1081	Db		AGTGACCTCTGTGTACACAGTGTTCGGCCCTGAGGACGTGGCCCTCATGTGGGGCTC	1140
1141	Qy		ATCGCCGTGGCCGTCTGCCTGGTCTCTGCTGTGTCTCATPCTCGTTTATTTGCCGG	1200
1141	Db		ATCGCCGTGGCCGTCTGCCTGGTCTCTGCTGTGTCTCATPCTCGTTTATTTGCCGG	1200
1201	Qy		AAGAGGAGGGGCTGGACTCAGATGCTGGCTGACTCGTCCATTTCTCACTCAGGCTCCAG	1260
1201	Db		AAGAGGAGGGGCTGGACTCAGATGCTGGCTGACTCGTCCATTTCTCACTCAGGCTCCAG	1260
1261	Qy		CCCGTCAAGCATCAAGCCCGACAAAGCAGACAAACCCCATCTGCTTCACCATCCACGCGGAC	1320

Db	13261	CCCCTCAGCATCAAGCCCGACCAAGCCGAGCAAAACCCCATCTGCTCAACATCCAGCCGGAC	13260
Qy	13321	CTCAGCACCAACCAACACACTACAGGCGAGTCTCTGTGCTCCCGCAGGATGGGCCCCAGC	13380
Db	13321	CTCAGCACCAACCAACCAACTACAGGCGAGTCTCTGTGCTCCCGCAGGATGGGCCCCAGC	13380
Qy	13381	CCCAGTTTCAGCTCACAATGGGCACTGTCTAGCCCCCTTGGTGGCGCGCCACACACA	14440
Db	13381	CCCAGTTTCAGCTCACAATGGGCACTGTCTAGCCCCCTTGGTGGCGCGCCACACACA	14440
Qy	14441	CTGCACCAACAGCTCTCCCACTCTGAGGCGAGGAGTTCTCTCCGCTCTCCACCCAG	15000
Db	14441	CTGCACCAACAGCTCTCCCACTCTGAGGCGAGGAGTTCTCTCCGCTCTCCACCCAG	15000
Qy	15011	AACTACTTCGCTCCCTGCCCGGAGGACACAGCAACTATGGGACCTTCAACTTC	15660
Db	15011	AACTACTTCGCTCCCTGCCCGGAGGACACAGCAACTATGGGACCTTCAACTTC	15660
Qy	15611	CTGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCATCCCTCCCGCAGATGCC	16220
Db	15611	CTGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCATCCCTCCCGCAGATGCC	16220
Qy	16211	ATACCCCGAGGAGATCTATGAGATCTACTCTCAGCTGCAACGCGGAGACGTGAGG	16880
Db	16211	ATACCCCGAGGAGATCTATGAGATCTACTCTCAGCTGCAACGCGGAGACGTGAGG	16880
Qy	16811	TTGGCCCTAGTGTGCTGTGACGCCCTGTGAGTCCCATCGTTAGCTGTGACCCCTTGGC	17440
Db	16811	TTGGCCCTAGTGTGCTGTGACGCCCTGTGAGTCCCATCGTTAGCTGTGACCCCTTGGC	17440
Qy	17411	GTCTGTCTACCCGCGCCAGTCACTCTGGCTATGGACCACTGTGGGAGCCAGCCCTGAC	18000
Db	17411	GTCTGTCTACCCGCGCCAGTCACTCTGGCTATGGACCACTGTGGGAGCCAGCCCTGAC	18000
Qy	18011	AGCTGGAGCTGTGCTCAAAAAGCACTGTGCGAGGCGACGTTGGGAGGATGTCTGCAC	18660
Db	18011	AGCTGGAGCTGTGCTCAAAAAGCACTGTGCGAGGCGACGTTGGGAGGATGTCTGCAC	18660
Qy	18611	CTGGGCGAGGAGGCGCCCTCCCACTTACTTGTCCAGCTGGAGGCGAGTGCCTGCTAC	19220
Db	18611	CTGGGCGAGGAGGCGCCCTCCCACTTACTTGTCCAGCTGGAGGCGAGTGCCTGCTAC	19220
Qy	19211	GTCTTTCACCGACGCTGGGCGGCTTTGCCCTGTGGGAGAGGCCCTCAGCGTGGCTGCC	19880
Db	19211	GTCTTTCACCGACGCTGGGCGGCTTTGCCCTGTGGGAGAGGCCCTCAGCGTGGCTGCC	19880
Qy	19811	GCGAAGCGCTCAAGCTGCTTCTTTTGGCGCGGTGGCGCTGCACCTCCCTCGAGTACAAC	20440
Db	19811	GCGAAGCGCTCAAGCTGCTTCTTTTGGCGCGGTGGCGCTGCACCTCCCTCGAGTACAAC	20440
Qy	20411	ATCCGGGTCTACTGCTTGCATGACACCCAGATGCACCTCAAGGAGTGTGTGCAGCTGGAG	21000
Db	20411	ATCCGGGTCTACTGCTTGCATGACACCCAGATGCACCTCAAGGAGTGTGTGCAGCTGGAG	21000
Qy	21011	AAGCAGCTGGGGGACAGCTGATCCAGGAGCGACGGGTCTCTGCACCTTCAAGGACAGTTAC	21660
Db	21011	AAGCAGCTGGGGGACAGCTGATCCAGGAGCGACGGGTCTCTGCACCTTCAAGGACAGTTAC	21660
Qy	21611	CACAACTGGGCTTATCCATCCAGATGTGCGCAGCTCCCTGTGGAAAGATGAAGCTCCTT	22220
Db	21611	CACAACTGGGCTTATCCATCCAGATGTGCGCAGCTCCCTGTGGAAAGATGAAGCTCCTT	22220
Qy	22211	GTACGCTACGAGGAGATCCCTTTTATCACTGTGGAATGGCACGACGGGTACTTGCAC	22880
Db	22211	GTACGCTACGAGGAGATCCCTTTTATCACTGTGGAATGGCACGACGGGTACTTGCAC	22880
Qy	22811	TGCACCTTTCACCTTGGAGCGTGTGAGCCCGACACTAGTGCCTTGCAGCTGTGG	23440
Db	22811	TGCACCTTTCACCTTGGAGCGTGTGAGCCCGACACTAGTGCCTTGCAGCTGTGG	23440
Qy	23411	GTGTGGCAGGTGGAGCGGCGACGGCAGAGCTTCAGCATCAACTTCAACACCAAGGAC	24000
Db	23411	GTGTGGCAGGTGGAGCGGCGACGGCAGAGCTTCAGCATCAACTTCAACACCAAGGAC	24000

QY 2401 ACAAGGTTTGCTGAGCTGCTGCTGCTGAGAGTGAAGCGGGGTCCTCCAGCGCTTGTGGGC 2460
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QY 2401 ACAAGGTTTGCTGAGCTGCTGCTGCTGAGAGTGAAGCGGGGTCCTCCAGCGCTTGTGGGC 2460
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DB |||||
QY 2521 CCTCTAGCGGGTGCCGACTGCGGAGCTCTGGCCGAGAACTCCACTTGGACAGCCAT 2580
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QY 2581 CTCAGCTTTTGGCTTCAAGCCAGCCAGCCAGCCAGCATGATCCTCAACTGTGGGAGCG 2640
DB |||||
QY 2581 CTCAGCTTTTGGCTTCAAGCCAGCCAGCCAGCCAGCATGATCCTCAACTGTGGGAGCG 2640
DB |||||
QY 2641 CGGCACTTTCCCAACCGGCAACTCAGCAGCTGGCTGCGAGCAGTGGCTGGAGTGGGCCAG 2700
DB |||||
QY 2641 CGGCACTTTCCCAACCGGCAACTCAGCAGCTGGCTGCGAGCAGTGGCTGGAGTGGGCCAG 2700
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QY 2701 CCAGAGCTGGCTCTTCAAGTGTGGAGGCTGAGTCTGAGGCGGCCAG 2752
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DB |||||

RESULT 2
AX451652
LOCUS AX451652 2697 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0233080.
ACCESSION AX451652
VERSION AX451652.1 GI:21698587
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
Koehler, R.H.
Regulation of human netrin binding membrane receptor unc5h-1
Patent: WO 0233080-A 1 25-APR-2002;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
1. .2697
/organism="Homo sapiens"
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ORIGIN
Query Match 97.7%; Score 2687.4; DB 6; Length 2697;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 46 ATGGCGCTGCGGCGCGGCTGTGGCCAGCGCTCTCTGGGCAATGCTCTGGCGCTTGGCTC 105
DB 1 ATGGCGCTGCGGCGCGGCTGTGGCCAGCGCTCTCTGGGCAATGCTCTGGCGCTTGGCTC 60

QY 106 CGCGGCTGCGGCGCGGCTGTGGCCAGCGCTCTGGGCAATGCTCTGGCGCTTGGCTC 165
DB 61 CGCGGCTGCGGCGCGGCTGTGGCCAGCGCTCTGGGCAATGCTCTGGCGCTTGGCTC 120

QY 166 GACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGGATGTGTACATGCTCAAGAACAGGCCA 225
DB 121 GACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGGATGTGTACATGCTCAAGAACAGGCCA 180

QY 226 GTGTGCTTGTGTGAAGCGCGTGTGGCCAGCGCTCTCTGGGCAATGCTCTGGCGCTTGGCTC 285
DB 181 GTGTGCTTGTGTGAAGCGCGTGTGGCCAGCGCTCTCTGGGCAATGCTCTGGCGCTTGGCTC 240

QY 286 TGCGTGGCCAGGTTGGACCACTGATCGAGCGGAGCAGACGCGGAGCAGTGGGCTGCC 345
DB 241 TGGGTGGCCAGGTTGGACCACTGATCGAGCGGAGCAGACGCGGAGCAGTGGGCTGCC 300

QY 346 ACCATGGAGTCCGCAATTAATGTCTCAAGGCGAGAGTTCGAGAAAGTGTCTCGGGCTGGAG 405
DB |||||
QY 301 ACCATGGAGTCCGCAATTAATGTCTCAAGGCGAGAGTTCGAGAAAGTGTCTCGGGCTGGAG 360
DB |||||
QY 406 GAAATACCTGCTGCTGAGTGTGGCATGAGAGTCTCTCGGGCACCAACAGAGTCAAGAGGCC 465
DB |||||
QY 361 GAAATACCTGCTGAGTGTGGCATGAGAGTCTCTCGGGCACCAACAGAGTCAAGAGGCC 420
DB |||||
QY 466 TACATCCGCTAGCAGATTGCGGCAAGAACTTCAGAGGAGGCGCTGGCCAGAGAGGTG 525
DB |||||
QY 421 TACATCCGCTAGCAGATTGCGGCAAGAACTTCAGAGGAGGCGCTGGCCAGAGAGGTG 480
DB |||||
QY 526 TCCCTGGAGCAGGAGCATGCTGCTCCCTGCGTCCACCGAGGGGATCCCTCCAGCCAG 585
DB |||||
QY 481 TCCCTGGAGCAGGAGCATGCTGCTCCCTGCGTCCACCGAGGGGATCCCTCCAGCCAG 540
DB |||||
QY 586 GTGAGTGGCTCCGGAACGAGGAGCTGTGTGAGACCCGCTCCCTGGACCCCAATGTATACATC 645
DB |||||
QY 541 GTGAGTGGCTCCGGAACGAGGAGCTGTGTGAGACCCGCTCCCTGGACCCCAATGTATACATC 600
DB |||||
QY 646 ACAGCGGAGCAGCAGCTGCTGGTGGGAGAGCCCGCTTGTGTGACAGCGGCCAATACATC 705
DB |||||
QY 601 ACAGCGGAGCAGCAGCTGCTGGTGGGAGAGCCCGCTTGTGTGACAGCGGCCAATACATC 660
DB |||||
QY 706 TGCCTGGCCAAAGAACTATGCTGGCAGCTGCGCGAGCGCTCCGCTGTGTGTATCGTCTAC 765
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QY 661 TGCCTGGCCAAAGAACTATGCTGGCAGCTGCGCGAGCGCTCCGCTGTGTGTATCGTCTAC 720
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QY 766 GTGAACCGTGGTGGTTCGAGCTGGAACGAGTGGTCCGCTCTGACGCGCGAGCTGTGGGCGC 825
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QY 721 GTGAACCGTGGTGGTTCGAGCTGGAACGAGTGGTCCGCTCTGACGCGCGAGCTGTGGGCGC 780
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QY 826 GGCTGGCAGAAACCGGAGCGGAGCTGCAACCAACCGGGGCGCTCTCAACGGGGGCGCTTTC 885
DB |||||
QY 781 GGCTGGCAGAAACCGGAGCGGAGCTGCAACCAACCGGGGCGCTCTCAACGGGGGCGCTTTC 840
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QY 886 TGTGAGGGGCAAGATGCTCCAGAAACAGCTTGCACCAACCGGGGCGCTCTCAACGGGGGCGCTTTC 945
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QY 946 TGAAGCCCGTGGAGCAAGTGTGGCTGTGGGCTGAGCTGCAACCACTGCGCGAGCGCT 1005
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QY 1066 ACCCGCAACTGTACAGTGACCTCTGTGTACACAGTGTCTTGGCCCTGAGGAGCTGGCC 1125
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QY 1021 ACCCGCAACTGTACAGTGACCTCTGTGTACACAGTGTCTTGGCCCTGAGGAGCTGGCC 1080
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QY 1081 CTCTATGTGGGCTCATATCGCGTGGCGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
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DB |||||
QY 1201 ACCTCAGGCTTCCAGCGCGCTCAGCATCAAGCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
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DB |||||
QY 1321 CAGATGGGCGGAGCGGCGGAGTTCAGCTCAACATGGGCGAGCTGTGTGTGTGTGTGTGTGTGT 1426
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1606 ATCCCCCAGATGCCATACCCCGAGGAGAGATCTATGATCTTACCTCAGCTGCACAAG 1665
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Qy
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1966 CTGAGCTGGCTGGCGCAAGCGCTCAAGCTGCTTCTGTTGGCGGCTGGCTGCACC 2025
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2086 GTGCTGAGCTGGAGAGCAGCTGGGCGGACAGCTGATCCAGAGCCACCGGCTCCTGCAC 2145
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2041 GTGCTGAGCTGGAGAGCAGCTGGGCGGACAGCTGATCCAGAGCCACCGGCTCCTGCAC 2100
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2146 TTCAAGGACAGTTACCAACCTGCGCTATCCATCCACGATGTGCCAGCTCCCTGTGG 2205
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2101 TTCAAGGACAGTTACCAACCTGCGCTATCCATCCACGATGTGCCAGCTCCCTGTGG 2160
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2206 AAGAGTAAAGCTCTTGTGAGTACAGAGATCCCTTTTATCAATCTGGAATGGCAGC 2265
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2161 AAGAGTAAAGCTCTTGTGAGTACAGAGATCCCTTTTATCAATCTGGAATGGCAGC 2220
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2266 CAGCGGTACTTGCACTGCACCTTCACTTGGAGGCTGTCAGCCCGCAGCACTAGTACCTG 2325
Db
2221 CAGCGGTACTTGCACTGCACCTTCACTTGGAGGCTGTCAGCCCGCAGCACTAGTACCTG 2280
Qy
2326 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACCGGGCAGAGCTTTCAGCATCAATTC 2385
Db
2281 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACCGGGCAGAGCTTTCAGCATCAATTC 2340
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2386 AACATCAAGGACACAAAGTTTGTGAGCTGTGCTGCTGTGAGAGTGAAGCGGGGTC 2445
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2686 GCTGGACTGGGCCAGCAGCAGCTGGCTCTTCCACAGTGTCCGAGGCTGAGTCTGA 2742
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RESULT 3
AX527916 2881 bp DNA linear PAT 21-NOV-2002
LOCUS
DEFINITION Sequence 1 from Patent WO0229038.
ACCESSION AX527916
VERSION AX527916.1 GI:25172359
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Herrmann, J.L., Rastelli, L. and Shinkets, R.A.
TITLE Novel proteins and nucleic acids encoding same and antibodies
directed against these proteins
JOURNAL Patent: WO 0229038-A 1 11-APR-2002;
Curagen Corporation (US)
FEATURES
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ORIGIN

Query Match 97.3%; Score 2676.4; DB 6; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

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Db 102 GGCTGTGGCAGCGCTCCTGGGCATAGTCTCGCGCTTGGCTCGCGGCTCGGGTGCC 161
Qy 121 CAGCAGATGCCACCGTGGCCAAACCCAGTGCCTGGTGCCAAACCCGACCTGCTTCCCAC 180
Db 162 CAGCAGATGCCACCGTGGCCAAACCCAGTGCCTGGTGCCAAACCCGACCTGCTTCCCAC 221
Qy 181 TTCTGTGGAGCCCCGAGGATGTATCATGTCAGATCTTCTTCAAGTGTAAACCGGAGTGGGTGCGCCAGGTG 240
Db 222 TTCTGTGGAGCCCCGAGGATGTATCATGTCAGTGTGTATCATGTCAGAAACAGGACGATGCTGTGTGTGC 281
Qy 241 AAGCGCTGTGCCCGCCAGCAGATCTTCTTCAAGTGTAAACCGGAGTGGGTGCGCCAGGTG 300
Db 282 AAGCGCTGTGCCCGCCAGCAGATCTTCTTCAAGTGTAAACCGGAGTGGGTGCGCCAGGTG 341
Qy 301 GACCACTGATTCAGCGCCAGCAGACAGCGGAGCAGTGGGTGCGCCACCATGAGAGTCCGC 360
Db 342 GACCACTGATTCAGCGCCAGCAGACAGCGGAGCAGTGGGTGCGCCACCATGAGAGTCCGC 401
Qy 361 ATTAATGTCTCAAGGAGCAGGTCGAGAGGTGCTTGGGCTGGAGGATTAATGTTGTCAG 420
Db 402 ATTAATGTCTCAAGGAGCAGGTCGAGAGGTGCTTGGGCTGGAGGATTAATGTTGTCAG 461
Qy 421 TGGCTGGCATGGAGCTCTCTCGGCGACCAACAGAGTCCAGAGGCCTACATCCGCGATAGCC 480
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Qy	2695	GGCCAGCCAGACGCTGGCGCTCTTCACAGTGTCCGAGGCTGAGTCTCAGGCGGCGCAG	2752
Db	2739	GGCCAGCCAGACGCTGGCGCTCTTCACAGTGTCCGAGGCTGAGTCTCAGGCGGCGCAG	2796
RESULT 4			
CQ730306			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
1			
REFERENCE			
AUTHORS			
TITLE			
Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.			
Kits, such as nucleic acid arrays, comprising a majority of			
humanexons or transcripts, for detecting expression and other uses			
thereof			
JOURNAL			
PE Corporation (NY) (US)			
Patent: WO 02068579-A 16240 06-SEP-2002;			
FEATURES			
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Query Match 88.5%; Score 2435.4; DB 6; Length 2784;			
Best Local Similarity 93.5%; Pred. No. 0;			
Matches 2646; Conservative 0; Mismatches 6; Indels 177; Gaps 3;			
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Db	61	CGCGGCTCGGTGCCAGCGAGTGCCACCGTGCCCAACCGAGTCTGTGCCAACCCG	120
Qy	166	GACCTGCTTCCCACTTCTGTGTGGAGCCGAGGATGTACATCGTCAAGAACAGCCA	225
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Qy	226	GTGCTGTGTGTGTCAGAGCGCGTCCCGCCACGAGATCTTCTTCAAGTGCAACGGGAG	285
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Qy	286	TGGGTGGCCAGGTGGACCACTGATCGAGCGCAGCAGACGGGAGCAGTGGGCTGCC	345
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Qy	466	TACATTCGCACTAGCAGATTTCGCAAGAACTTCGAGCAGGAGCGCTGGCCCAAGAGGTG	525
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Qy	526	TCCCTGAGCAGGGCATCGTCTGCCCTTCGCGTCCACCGGAGGGCATCCCTCCAGCCGAG	585
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LOCUS AX367094 3580 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0198354.
ACCESSION AX367094
VERSION AX367094.1 GI:18855296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B.,
Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,
Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,
Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and
Sanjanwala,M.S.
RECEPTORS
Patent: WO 0198354-A 13 27-DEC-2001;
Incyte Genomics, Inc. (US)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN
Query Match 85.6%; Score 2356; DB 6; Length 3580;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;
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DEFINITION	Mus musculus mRNA for netrin receptor Uncsh1 linear ROD 24-SEP-2002
ACCESSION	AJ487852
VERSION	AJ487852.1 GI:22035783
KEYWORDS	netrin receptor Uncsh1; Uncsh1 gene.
SOURCE	Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS
Engelkamp, D.

TITLE	Cloning of three mouse Unc5 genes and their expression patterns at mid-gestation
JOURNAL	Mech. Dev. 118 (1-2), 191-197 (2002)
MEDLINE	22239710
PUBMED	12351186
REFERENCE	2 (bases 1 to 3992)


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RESULT 8
LOCUS AX268596 2697 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 15 from Patent WO0175440.
ACCESSION AX268596
VERSION AX268596.1 GI:16541710
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and
AUTHORS Pratt,J.Y.
TITLE Schizophrenia related genes
JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;
WELFIDE CORPORATION (JP)
FEATURES
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ORIGIN
Query Match 81.8%; Score 2252.2; DB 6; Length 2697;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

Qy 46 ATGCCGCTCCGGCCCGCTGTGGCCAGCGCTCTCGGCGATAGTCTCGCGCTTGGCTC 105
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ORIGIN

Query Match 81.8%; Score 2252.2; DB 10; Length 2697;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

Qy	46	ATGCGCGTCCGGCCCGCGCTGTGGCCAGCGCTCTGGGCATAGTCCTCGCGCTGGCTC	105
Db	1	ATGCGCGTCCGGCCCGCGCTGTGGCCAGCGCTCTGGGCATAGTCCTCGCGCGCTGGCTT	60
Qy	106	CGCGGCTCGGGTCCCAAGCAGAGTCCACCGTGGCCCAACCCAGTGCCTGTGGCCAAACCCG	165
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Db	241	TGGGTCCGCGAGTCGATCAGTAAATTGAACGACAGCCAGCACAGCGGATTCGCA	300
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RESULT 10
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DEFINITION Mus musculus unc-5 homolog A (C. elegans), mRNA (cdna clone
MGC:66671 IMAGE:6813463), complete cds.
ACCESSION BC058084
VERSION BC058084.1 GI:34784158
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3844)
AUTHORS Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusik, K., Farmer, A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.B.,
Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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2 (bases 1 to 3844)
Strausberg, R.
Direct Submission
Submitted (08-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Nees, Pawan Pandoh, Anna-Lisea Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
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This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 23346570.
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RESULT 11
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IMAGE:4126760), partial cds.
ACCESSION BC009333
VERSION BC009333.2
KEYWORDS GI:40226527
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
REFERENCE 1 (bases 1 to 2688)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vallalao, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shavchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smillius, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2688)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2001) National Institutes of Health, Mammalian
PUBMED Gene Collection (MGC), Cancer Genomics Office, National Cancer
REFERENCE Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NTH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT On Dec 19, 2003 this sequence version replaced gi:14424611.
Contact: MGC help desk
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhater, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
McDowell, J., Masello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowall, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Taurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAL Plate: 26 Row: g Column: 22.
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DEFINITION Sequence 91 from Patent WO0073328.
ACCESSION AX054976
VERSION AX054976.1 GI:12228344

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE

1 van Criekeing, W., Roelens, I., Bogaert, T. and Verwaerde, P.
Unc-5 constructs and screening methods
Patent: WO 0073328-A 91 07-DEC-2000;
Devgen NV (BB)

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RESULT 14

MMU72634
LOCUS MMU72634 9299 bp mRNA linear ROD 13-MAY-1997
DEFINITION Mus musculus rostral cerebellar malformation protein (rcm) mRNA,
complete cds.
ACCESSION U72634
VERSION U72634.1 GI:2088526

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 9299)

Ackerman, S.L., Kozak, L.P., Przyborski, S.A., Rund, L.A., Boyer, B.B.

and Knowles, B.B.

The mouse rostral cerebellar malformation gene encodes an

UNC-5-like protein

Nature 386 (6627), 838-842 (1997)

97271898

PUBMED

2 (bases 1 to 9299)

Ackerman, S.L., Kozak, L.P., Rund, L.A. and Knowles, B.B.

Direct Submission

Submitted (25-SEP-1996) The Jackson Laboratory, 600 Main Street,

Bar Harbor, ME 04609, USA

FEATURES

source

Location/Qualifiers

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151..2946

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ORIGIN

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Best Local Similarity 62.7%; Pred. No. 1.5e-156;

Matches 1660; Conservative 0; Mismatches 925; Indels 63; Gaps 5;

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RESULT 15
AY187310
LOCUS
DEFINITION
Gallus gallus UNC5-like protein 3 mRNA, complete cds.
ACCESSION
AY187310
VERSION
AY187310.1 GI:31442350
KEYWORDS
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 2962)
Guan,W. and Condic,M.L.
Characterization of Netrin-1, Neogenin and cUNC-5H3 expression
during chick dorsal root ganglia development
Gene Expr. Patterns 3, 369-373 (2003)
REFERENCE
2 (bases 1 to 2962)
Guan,W. and Condic,M.L.
Direct Submission
Submitted (26-NOV-2002) Neurobiology & Anatomy, University of Utah,
20 North, 1900 East, Salt Lake City, UT 84132-3401, USA
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Query Match

36.0%; Score 991; DB 5; Length 2962;

ORIGIN

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Db	2729	CAGCAGTCTGGAAAGAAATGGGACGACATGAAC	2788
Qy	2735	AGTCTGAGGCCCGC	2749
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Search completed: August 7, 2005, 18:37:25
Job time : 19367 secs

Result No.	Query			DB	ID	Description
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6	2674.8	97.2	2881	12	ADH71649	Adh71649 Human ge
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XX Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX WPI: 2002-180074/23.
DR P-PSDB; AAU85403.
XX
PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX
XX Claim 9; Page 9-10; 213pp; English.
XX
CC The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, hematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence encodes a
CC NOVX protein
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;
Query Match
Best Local Similarity 100.0%; Score 2752; DB 6; Length 2752;
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCGCGGGCCCGCGCCCGCGCCCGCGCCCGCGCCCGCGCGCATGGCGCCGCGCC 60
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Db 241 AAGCCGTGCCCCGACGCGAGATCTTCTCAAGTGCACCGGGAGTGGGCGGCCAGGTG 300
Qy 301 GACCACGTGATTCGAGCGCAGCAGACAGCGGAGCAGTGGGTGCCCCACCATGGAGGTCCGC 360
Db 301 GACCACGTGATTCGAGCGCAGCAGACAGCGGAGCAGTGGGTGCCCCACCATGGAGGTCCGC 360
Qy 361 ATTAATGTCTCAAGGACGAGGTGTGAGAGGTGTTCGGGTGTGGAGGAATATCTGGTCCAG 420
Db 361 ATTAATGTCTCAAGGACGAGGTGTGAGAGGTGTTCGGGTGTGGAGGAATATCTGGTCCAG 420
Qy 421 TGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCGCTACATCCGCGATAGCC 480
```

Db 1501 AACTACTTCCTCCCTCCCTCCCGGACACAGCAACATGACCTATGGACCTTCAACTTC 1560
Qy 1561 CTGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCCTCTCATCCCCCAGATGCC 1620
Db 1561 CTGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCCTCTCATCCCCCAGATGCC 1620
Qy 1621 ATACCCCGAGGGAAGATCTATGAGATCTTACCTGCTGCAAAAGCCGGAAGAGCGTGAGG 1680
Db 1621 ATACCCCGAGGGAAGATCTATGAGATCTTACCTGCTGCAAAAGCCGGAAGAGCGTGAGG 1680
Qy 1681 TTGGCCCTTAGCTGGCTGTCAGACCTGCTGAGTCCCATCTGTTAGCTGTGGACCCCTGGC 1740
Db 1681 TTGGCCCTTAGCTGGCTGTCAGACCTGCTGAGTCCCATCTGTTAGCTGTGGACCCCTGGC 1740
Qy 1741 GTCTGCTCACCCGCGCCAGTCACTCTGGCTATGACCACTGTGGGAGCCAGCCCTGAC 1800
Db 1741 GTCTGCTCACCCGCGCCAGTCACTCTGGCTATGACCACTGTGGGAGCCAGCCCTGAC 1800
Qy 1801 AGCTGGAGCCTGCGCTCAAAAAGAGTCGTGCGAGGCGAGCTGGGAGGATGTGCTGCAC 1860
Db 1801 AGCTGGAGCCTGCGCTCAAAAAGAGTCGTGCGAGGCGAGCTGGGAGGATGTGCTGCAC 1860
Qy 1861 CTGGCGGAGGAGGCGCTCCCACTCTACTACTGCGAGCTGGAGGCGAGCTGCTGTAC 1920
Db 1861 CTGGCGGAGGAGGCGCTCCCACTCTACTACTGCGAGCTGGAGGCGAGCTGCTGTAC 1920
Qy 1921 GTCTTCCCGAGCAGCTGGGCGCTTTTGCCCTGTGGGAGGCGCTCAGCGTGGCTGCC 1980
Db 1921 GTCTTCCCGAGCAGCTGGGCGCTTTTGCCCTGTGGGAGGCGCTCAGCGTGGCTGCC 1980
Qy 1981 GCCAAGCGCCTCAAGCTGCTTCTGTTGCGCGGCTGCTGCTCCTCGAGTACAAC 2040
Db 1981 GCCAAGCGCCTCAAGCTGCTTCTGTTGCGCGGCTGCTGCTCCTCGAGTACAAC 2040
Qy 2041 ATCCGGTCTACTGCTGATGACACCCAGCTGCTCAAGGAGGTGCTGCTGAG 2100
Db 2041 ATCCGGTCTACTGCTGATGACACCCAGCTGCTCAAGGAGGTGCTGCTGAG 2100
Qy 2101 AAGCAGCTGGGGGAGCAGCTGATCAGGAGCAGGGTCTGCTCAAGGAGCAGTTAC 2160
Db 2101 AAGCAGCTGGGGGAGCAGCTGATCAGGAGCAGGGTCTGCTCAAGGAGCAGTTAC 2160
Qy 2161 CACAACCTGCGCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAACTCCTT 2220
Db 2161 CACAACCTGCGCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAACTCCTT 2220
Qy 2221 GTGAGCTACGAGATGCTCCCTTTTATCAGATCTGGAATGSCAGCGGCTACTGCAC 2280
Db 2221 GTGAGCTACGAGATGCTCCCTTTTATCAGATCTGGAATGSCAGCGGCTACTGCAC 2280
Qy 2281 TGCACTTTCACTGGAGCGTGTGAGCCCGAGCAGCTAGTACCTGGCTGCAAGCTGTGG 2340
Db 2281 TGCACTTTCACTGGAGCGTGTGAGCCCGAGCAGCTAGTACCTGGCTGCAAGCTGTGG 2340
Qy 2341 GTGTGGCAGGTGGAGGCGAGCGGCGAGAGTTCAGCATCACTTCAACATCACCAGGAC 2400
Db 2341 GTGTGGCAGGTGGAGGCGAGCGGCGAGAGTTCAGCATCACTTCAACATCACCAGGAC 2400
Qy 2401 ACAAGGTTTGTGAGCTGCTGGCTCTGAGAGTGAAGGGGGTCCAGCCTGGTGGC 2460
Db 2401 ACAAGGTTTGTGAGCTGCTGGCTCTGAGAGTGAAGGGGGTCCAGCCTGGTGGC 2460
Qy 2461 CCAGTGTCTCAAGATCCCTTCTCATTCGGGAGAGATATTTCCAGCTGGACCCCA 2520
Db 2461 CCAGTGTCTCAAGATCCCTTCTCATTCGGGAGAGATATTTCCAGCTGGACCCCA 2520
Qy 2521 CCCTGTAGGGGGTGGCGAGTGGCGGACTCTGGCCAGAACTCCACCTGGAGCAGCAT 2580
Db 2521 CCCTGTAGGGGGTGGCGAGTGGCGGACTCTGGCCAGAACTCCACCTGGAGCAGCAT 2580
Qy 2581 CTGAGCTTCTTTGCTCCAGCCCGAGCCCGAGCCCATGATCTCAACCTGTGGAGGCG 2640
Db 2581 CTGAGCTTCTTTGCTCCAGCCCGAGCCCGAGCCCATGATCTCAACCTGTGGAGGCG 2640

Qy 2641 CGGCACCTTCCCAACGCAACCTCAGCAGCTGGCTGCGAGCTGGCTGGACTGGCCAG 2700
Db 2641 CGGCACCTTCCCAACGCAACCTCAGCAGCTGGCTGCGAGCTGGCTGGACTGGCCAG 2700
Qy 2701 CCAGACGCTGGCTCTTTTACAGTGTGCGAGGCTGAGTGTGAGCCCGGCCAG 2752
Db 2701 CCAGACGCTGGCTCTTTTACAGTGTGCGAGGCTGAGTGTGAGCCCGGCCAG 2752
RESULT 2
ADH71617
ID ADH71617 standard; DNA; 2752 BP.
XX AC ADH71617;
XX AC ADH71617;
DT 25-MAR-2004 (first entry)
XX Human gene of the invention NOV21e SEQ ID NO:513.
ds; gene; human; cytostratic; immunomodulator; neuroprotective; nootropic;
anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
obesity; diabetes; infectious disease; metabolic syndrome X;
dyslipidaemia.
XX Homo sapiens.
OS Homo sapiens.
XX WO2003102155-A2.
PD 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.

PF 15-OCT-2001; 2001WO-EP011891.
XX
PR 16-OCT-2000; 2000US-0240061P.
XX
XX (PARB) BAYER AG.
PA
XX
XX Koehler RH;
PI
XX WPI; 2002-463314/49.
XX
XX P-PSDB; AAU97899.
DR
XX
XX Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.
XX
XX Claim 1; Fig 1; 94pp; English.
PS
XX
CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents a DNA sequence encoding the
CC human netrin binding membrane receptor UNC5H-1 protein of the invention
XX
XX
SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Query Match 97.7%; Score 2687.4; DB 6; Length 2697;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 46 ATGGCGTCCGGCCCGCGCTGTGCGCAGAGTGCCACCGTGCCCAACCCAGTCCCTGGCGCTTGCTC 105
DB 1 ATGGCCGTTCGGCCCGCGCTGTGCGCAGAGTGCCACCGTGCCCAACCCAGTCCCTGGCGCTTGCTC 60

QY 106 CGCGGCTCGGTGCCAGAGTGCCACCGTGCCCAACCCAGTCCCTGGTGCCCAACCCG 165
DB 61 CGCGGCTCGGTGCCAGAGTGCCACCGTGCCCAACCCAGTCCCTGGTGCCCAACCCG 120

QY 166 GACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACCAAGCCA 225
DB 121 GACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACCAAGCCA 180

QY 226 GTGCTGCTGTGTGTCAGAGCCGCTGCCCGCAGCAGATCTTCTTCAAGTGCAACGGGGAG 285
DB 181 GTGCTGCTGTGTGTCAGAGCCGCTGCCCGCAGCAGATCTTCTTCAAGTGCAACGGGGAG 240

QY 286 TGGGTGGCGCAGGTGGACCACTGATCGAGCGCAGCAGACAGCGGAGCAGTGGGCTGCC 345
DB 241 TGGGTGGCGCAGGTGGACCACTGATCGAGCGCAGCAGACAGCGGAGCAGTGGGCTGCC 300

QY 346 ACCATGAGGTCCGCATTAATGTCTCAAGGAGCAGGTTCGAGAAAGTGTTCGGGCTGGAG 405
DB 301 ACCATGAGGTCCGCATTAATGTCTCAAGGAGCAGGTTCGAGAAAGTGTTCGGGCTGGAG 360

QY 406 GAATACTGGTCCAGTGGGTGGATGGAGTCCCTCGGGCACCACCAAGAGTCAAGAGGCC 465
DB 361 GAATACTGGTCCAGTGGGTGGATGGAGTCCCTCGGGCACCACCAAGAGTCAAGAGGCC 420

QY 466 TACATCCGCATAGCCAGATTTCGCAAGAACTTCGAGCAGAGGCGCTGGCCCAAGAGGTG 525
DB 466 TACATCCGCATAGCCAGATTTCGCAAGAACTTCGAGCAGAGGCGCTGGCCCAAGAGGTG 560

421 TACATCCGCATAGCCATTTCGCGCAAGAACTTCGAGCAGAGGCGCTGGCCCAAGAGGTG 480
526 TCCTTGGAGCAGGGGCATTCGTGCTGCCCTGCCCTCCACCGGAGGGGCATTCCTTCCAGCCGAG 585
481 TCCTTGGAGCAGGGGCATTCGTGCTGCCCTGCCCTCCACCGGAGGGGCATTCCTTCCAGCCGAG 540
586 GTGGAGTGGCTCCGGAAACGAGGACCTGGTGGACCGCTCCCTGGACCCCAATGTATATCATC 645
541 GTGGAGTGGCTCCGGAAACGAGGACCTGGTGGACCGCTCCCTGGACCCCAATGTATATCATC 600
646 ACCGGGAGCAGACAGCTGGTGGTGGACAGCGCGCTTCCTGTCACACGGCAACTACACC 705
601 ACCGGGAGCAGACAGCTGGTGGTGGACAGCGCGCTTCCTGTCACACGGCAACTACACC 660
706 TGGGTGGCCCAAGAACATTCGTGGCACTGCGCGCAGCGCTCCCTGCTGTCATCGTCTAC 765
661 TGGGTGGCCCAAGAACATTCGTGGCACTGCGCGCAGCGCTCCCTGCTGTCATCGTCTAC 720
766 GTGAAACGCTGGGTGGTGGACCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 825
721 GTGAAACGCTGGGTGGTGGACCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
826 GGCTTGGCAGAAACGAGCGCGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTC 885
781 GGCTTGGCAGAAACGAGCGCGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTC 840
886 TGTGAGGGGCGAGTAATTCAGAGAAACAGCCTGCGGCCACCTGTGCGCCAGTAGACGGCAGC 945
841 TGTGAGGGGCGAGTAATTCAGAGAAACAGCCTGCGGCCACCTGTGCGCCAGTAGACGGCAGC 900
946 TGGAGCCCGTGGAGCAAGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1005
901 TGGAGCCCGTGGAGCAAGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 960
1006 GAGTGTCTCTACCCAGCAGCAGCCCGCCAGCGAGGAGTGCCAGGGGCACTGACCTGGAC 1065
961 GAGTGTCTCTACCCAGCAGCAGCCCGCCAGCGAGGAGTGCCAGGGGCACTGACCTGGAC 1020
1066 ACCGCGAACTGTATACAGTGAACCTCTGTGTACA CAGTGTCTTCTGGCCCTTGAGGAGCTGG 1125
1021 ACCGCGAACTGTATACAGTGAACCTCTGTGTACA CAGTGTCTTCTGGCCCTTGAGGAGCTGG 1080
1126 CTCTATGTGGGCTCATCGCCGCTGGCCGCTGCTGCTGGTCTGCTGCTGCTGCTGCTCATC 1185
1081 CTCTATGTGGGCTCATCGCCGCTGGCCGCTGCTGCTGGTCTGCTGCTGCTGCTGCTCATC 1140
1186 CTCTATTTATTTGCGGAGAGAGGGGCTGGAGTCTCAGATGTGGTGTGACTGCTGCTCATTTCTC 1245
1141 CTCTATTTATTTGCGGAGAGAGGGGCTGGAGTCTCAGATGTGGTGTGACTGCTGCTCATTTCTC 1200
1246 ACCTCAGGCTTTCAGGCCGCTCAGGATCAAGCCAGCAAGAAAGAGACAAACCCCATCTGCTC 1305
1201 ACCTCAGGCTTTCAGGCCGCTCAGGATCAAGCCAGCAAGAAAGAGACAAACCCCATCTGCTC 1260
1306 ACCATCCAGCGGAGCCTCAGCAGCAGCCACCAACCACTACCCAGGCGAGTCTCTGTCCTCCGG 1365
1261 ACCATCCAGCGGAGCCTCAGCAGCAGCCACCAACCACTACCCAGGCGAGTCTCTGTCCTCCGG 1320
1366 CAGGATGGGCGCAGCCCAAGTTCCAGTCAACAAATGGGCACTGTCTCAGCCCCCTCGGT 1425
1321 CAGGATGGGCGCAGCCCAAGTTCCAGTCAACAAATGGGCACTGTCTCAGCCCCCTCGGT 1380
1426 GGCGGCGCCACACATCTGACACAGCTCTCCACCTCTGAGGGCCGAGGAGTTCGTCTCC 1485
1381 GGCGGCGCCACACATCTGACACAGCTCTCCACCTCTGAGGGCCGAGGAGTTCGTCTCC 1440
1486 CGCTCTCTCAACCCAGAACTACTTCCGCTCCCTGCGCGGAGCAGCAGCAACATGACCTAT 1545
1441 CGCTCTCTCAACCCAGAACTACTTCCGCTCCCTGCGCGGAGCAGCAGCAACATGACCTAT 1500
1546 GGGAACCTTCAACTTCCTCGGGGGCGCGCTGATGATCCCTAATACAGGTATCAGCCTCTC 1605
1501 GGGAACCTTCAACTTCCTCGGGGGCGCGCTGATGATCCCTAATACAGGAAATCAGCCTCTC 1560

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QY 1606 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACTCACCCTGCACAAG 1665
Db 1561 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACTCACCCTGCACAAG 1620
QY 1666 CCGAAGACGTGAGGTTCCCTAGCTGCTGTGTGAGACCCCTGCTGAGTCCCATCGTTAGC 1725
Db 1621 CCGAAGACGTGAGGTTCCCTAGCTGCTGTGTGAGACCCCTGCTGAGTCCCATCGTTAGC 1680
QY 1726 TGTGAGCCCCCTGGGCTCCTGCTCACCGGCCAGTTCATCTCTGGCTATGAGACCATGTGGG 1785
Db 1681 TGTGAGCCCCCTGGGCTCCTGCTCACCGGCCAGTTCATCTCTGGCTATGAGACCATGTGGG 1740
QY 1786 GAGCCAGCCTGACAGCTGGAGCTGCGCTCAAAAGACAGTCTGTGAGGGGAGCTGG 1845
Db 1741 GAGCCAGCCTGACAGCTGGAGCTGCGCTCAAAAGACAGTCTGTGAGGGGAGCTGG 1800
QY 1846 GAGGATGTGTCACCTGGGCGAGAGGCGCCCTCCACCTCTACTACTGTCCAGCTGGAG 1905
Db 1801 GAGGATGTGTCACCTGGGCGAGAGGCGCCCTCCACCTCTACTACTGTCCAGCTGGAG 1860
QY 1906 GCCAGTGCCTGCTAGCTCTTACCGAGCAGCTGGGCGCGCTTGTGCTGTGGGAGAGGCC 1965
Db 1861 GCCAGTGCCTGCTAGCTCTTACCGAGCAGCTGGGCGCGCTTGTGCTGTGGGAGAGGCC 1920
QY 1966 CTCAGCGTGGCTGCGGCCAAGCGCTCAAGCTGCTTCTGTTTGGCGGCTGCGCTGCACC 2025
Db 1921 CTCAGCGTGGCTGCGGCCAAGCGCTCAAGCTGCTTCTGTTTGGCGGCTGCGCTGCACC 1980
QY 2026 TCCCTCGAGTAAACATCCCGGCTTACTGCTGCAATGACACCCACGATGCACTCAAGGAG 2085
Db 1981 TCCCTCGAGTAAACATCCCGGCTTACTGCTGCAATGACACCCACGATGCACTCAAGGAG 2040
QY 2086 GTGCTGAGCTGGAGAGCAGCTGGGGGAGCAGCTGATCCAGAGCCACCGGCTCTGCAC 2145
Db 2041 GTGCTGAGCTGGAGAGCAGCTGGGGGAGCAGCTGATCCAGAGCCACCGGCTCTGCAC 2100
QY 2146 TTCAGAGACAGTATACCAACCTGCGCTTATCCATCCACGATGTGCCAGCTCCCTGTGG 2205
Db 2101 TTCAGAGACAGTATACCAACCTGCGCTTATCCATCCACGATGTGCCAGCTCCCTGTGG 2160
QY 2206 AAGAGTAAGCTCTTGTGTCAGTACAGAGAGATCCCTTTTATCATCATCTGGAATGGCAGC 2265
Db 2161 AAGAGTAAGCTCTTGTGTCAGTACAGAGAGATCCCTTTTATCATCATCTGGAATGGCAGC 2220
QY 2266 CAGCGGTACTTGCATGCACTTACCTTACCTTGAGGCTGTACGCCCCAGCACTAGTACCTG 2325
Db 2221 CAGCGGTACTTGCATGCACTTACCTTACCTTGAGGCTGTACGCCCCAGCACTAGTACCTG 2280
QY 2326 GCCTGCAAGCTGTGGGTGTGTCAGGTGGAGGGCCAGCGGACAGAGCTTTCAGCATCAACTTC 2385
Db 2281 GCCTGCAAGCTGTGGGTGTGTCAGGTGGAGGGCCAGCGGACAGAGCTTTCAGCATCAACTTC 2340
QY 2386 AACATCAACCAAGSACAAAGTTTGTGAGCTGTGCTCTGGAGAGTGAAGCGGGGTC 2445
Db 2341 AACATCAACCAAGSACAAAGTTTGTGAGCTGTGCTCTGGAGAGTGAAGCGGGGTC 2400
QY 2446 CCAGCCCTGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATCTCGCAGAGATTAATT 2505
Db 2401 CCAGCCCTGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATCTCGCAGAGATTAATT 2460
QY 2506 TCCAGCTGGACCCACCTGTAGGCGGGTCCGACTGGGCGGACTCTGGGCCCAAGAACTC 2565
Db 2461 TCCAGCTGGACCCACCTGTAGGCGGGTCCGACTGGGCGGACTCTGGGCCCAAGAACTC 2520
QY 2566 CACTTGAGACCCATCTCAGCTTCTTTGCTTCCAAAGCCCCAGCCCCACAGCCATGATCCTC 2625
Db 2521 CACTTGAGACCCATCTCAGCTTCTTTGCTTCCAAAGCCCCAGCCCCACAGCCATGATCCTC 2580
QY 2626 AACCTGTGGGAGGCGCGCACTTCCCCNAAAGGCAACCTCAGCCAGCTGTGGTGCAGCAGTG 2685
Db 2581 AACCTGTGGGAGGCGCGCACTTCCCCNAAAGGCAACCTCAGCCAGCTGTGGTGCAGCAGTG 2640
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QY 2686 GCTGCACTGGGCGCCAGCAGCGCTGGCTCTTTCACAGTGTGGAGGCTGAGTGTCTGA 2742
Db 2641 GCTGCACTGGGCGCCAGCAGCGCTGGCTCTTTCACAGTGTGGAGGCTGAGTGTCTGA 2697

RESULT 4
ID ABK49422 standard; DNA; 2881 BP.
XX
AC ABK49422;
XX
DT 15-JUL-2002 (first entry)
XX
DE DNA encoding human UNC5-like protein NOV1.
XX
KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
chromosome 13; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 87..2786
FT /*tag= a
FT /product= "Human UNC5-like protein NOV1"
XX
PN WO200229038-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031377.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Herrmann JL, Rastelli L, Shimkets RA;
XX
DR WPI; 2002-340104/37.
XX
DR P-PSDB; AAU79939.
XX
PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
treating cardiomyopathy, atherosclerosis, and cancer.
XX
PS Claim 8; Page 7-8; 180pp; English.
XX
CC The present invention relates to a new NOVX polypeptide having a 900
(NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
residue amino acid sequence, as given in the specification. The novel
polypeptide, and its encoding polynucleotide, are used to treat
cardiomyopathy, atherosclerosis, cancer or a disease related to cell
signal processing and metabolic pathway modulation, in a human. Detecting
the polypeptide or polynucleotide is useful for identifying cancerous
tissue. The antibody can be used to treat diabetes or cancer. The host
cells can be used to produce non-human transgenic animals useful in drug
screening. The present nucleic acid sequence is that of the human UNC5-
like NOV1 gene located on chromosome 13. This sequence encodes the human
UNC5-like protein NOV1 of the invention
XX
SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Query Match 97.3%; Score 2676.4; DB 6; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

QY 1 CCGCGGGGGCCCCCGCGCCCGCGCTGCGCCCGCGCCCGCATGGCCGTCCGCGCCC 60
Db 42 CCGCGGGGGCCCCCGCGCCCGCGCCCGCGCTGCGCCCGCGCGCATGGCCGTCCGCGCCC 101
QY 61 GGCTGTGGGCAGCGTCTCTGGGCATAGTCTCTGCCGCTTGGCTCCCGCGCTCGGCTGCC 120
Db 102 GGCTGTGGGCAGCGTCTCTGGGCATAGTCTCTGCCGCTTGGCTCCCGCGCTCGGCTGCC 161
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Qy	121	CAGCAGAGTGCACCGTGGCCAAACCCAGTGCCTGGTGCACAAACCGGAGCCTGCTTCCCCAC	180
Db	162	CAGCAGAGTGCACCGTGGCCAAACCCAGTGCCTGGTGCACAAACCGGAGCCTGCTTCCCCAC	221
Qy	181	TTCTCTGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAGCCAGTGTGCTGTGTGC	240
Db	222	TTCTCTGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAGCCAGTGTGCTGTGTGC	281
Qy	241	AAGGCCGTGGCCCGCACCGCAGATCTTCTTCAAGTGCACACGGGGAGTGGGTGCGCCAGGTG	300
Db	282	AAGGCCGTGGCCCGCACCGCAGATCTTCTTCAAGTGCACACGGGGAGTGGGTGCGCCAGGTG	341
Qy	301	GACACATGATCGAGCGCAGCAGACAGCGGAGCAGTGGGTGCCCAACATGAGAGTCCGC	360
Db	342	GACACATGATCGAGCGCAGCAGACAGCGGAGCAGTGGGTGCCCAACATGAGAGTCCGC	401
Qy	361	ATTAAATGTCTCAAGSCAGCAGTGCAGAGAGTGTTCGGGCTGGAGGAATACTGGTGCCAG	420
Db	402	ATTAAATGTCTCAAGSCAGCAGTGCAGAGAGTGTTCGGGCTGGAGGAATACTGGTGCCAG	461
Qy	421	TGCGTGGCATGGAGTCTCTCGGGCACCACCAAGAGTCAGAGGCTTACATCCGCGATAGCC	480
Db	462	TGCGTGGCATGGAGTCTCTCGGGCACCACCAAGAGTCAGAGGCTTACATCCGCGATAGCC	521
Qy	481	AGATTGGCAAGAACTTCGAGCAGGAGCGCGTGGCCAAAGAGTGTCCCTGGAGCAGGGC	540
Db	522	AGATTGGCAAGAACTTCGAGCAGGAGCGCGTGGCCAAAGAGTGTCCCTGGAGCAGGGC	581
Qy	541	ATCGTGTGCCCTGCCGTGCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGTGCTCCGG	600
Db	582	ATCGTGTGCCCTGCCGTGCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGTGCTCCGG	641
Qy	601	AACGAGGACCTGTGAGCCCGTCCCTGGACCCCAATGTATACATCACGCGGAGCAGCAGC	660
Db	642	AACGAGGACCTGTGAGCCCGTCCCTGGACCCCAATGTATACATCACGCGGAGCAGCAGC	701
Qy	661	CTGTGTGTGGACAGGCGCGCTTGTGTGACACGGCCAACTACATCTGCTGGCCCAAGAAC	720
Db	702	CTGTGTGTGGACAGGCGCGCTTGTGTGACACGGCCAACTACATCTGCTGGCCCAAGAAC	761
Qy	721	ATCGTGGCAGCTGCCCGCAGCGCTCCGCTGTCTGTCTATCTGTCTACGTGAACGCTGGGTGG	780
Db	762	ATCGTGGCAGCTGCCCGCAGCGCTCCGCTGTCTGTCTATCTGTCTACGTGAACGCTGGGTGG	821
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGACGCCCAAGCTGTGGCGCGCTGGCAGAAACGG	840
Db	822	TCGACGTGGACCGAGTGGTCCGTCTGACGCCCAAGCTGTGGCGCGCTGGCAGAAACGG	881
Qy	841	AGCCGGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT	900
Db	882	AGCCGGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT	941
Qy	901	GTCCAGAA---AACAGCTGCGCCACCCCTGTGCCAGTAGACGGCAGCTGAGAGCCCGTGG	957
Db	942	GTCCATGACCGCACCGTCTCTCTCTGTCTGTCTGTGTGAGCGCAGCTGGAGCCCGTGG	1001
Qy	958	AGCAAGTGGTGGCGCTGTGGCTGGAATGACCCCACTGGCGGAGCCGTGAGTGTCTGAC	1017
Db	1002	AGCAAGTGGTGGCGCTGTGGCTGGAATGACCCCACTGGCGGAGCCGTGAGTGTCTGAC	1061
Qy	1018	CCAGCACCCCGCAACCGAGGGGAGGTGCGAGGGCACTGACCTGGACACCCCGCACTGT	1077
Db	1062	CCAGCACCCCGCAACCGAGGGGAGGTGCGAGGGCACTGACCTGGACACCCCGCACTGT	1121
Qy	1078	ACCAGTGACCTCTGTGTACAGTGTCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1137
Db	1122	ACCAGTGACCTCTGTGTACAGTGTCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1181
Qy	1138	CTCATCCCGTGGCCGTCTGCTGGTCTGCTGTGCTGTGCTGTCTCATCTCGTGTATTGC	1197
Db	1182	CTCATCCCGTGGCCGTCTGCTGGTCTGCTGTGCTGTGCTGTCTCATCTCGTGTATTGC	1241

Qy	1198	CGGAAGAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCCTCAGGGCTTC	1257
Db	1242	CGGAAGAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCCTCAGGGCTTC	1301
Qy	1258	CAGCCGTGAGCATCAAGCCCAAGCAGACAAACCCCATCTGTCTCACCATTCCAGCCG	1317
Db	1302	CAGCCGTGAGCATCAAGCCCAAGCAGACAAACCCCATCTGTCTCACCATTCCAGCCG	1361
Qy	1318	GACCTCAGCACACCAACCACTACCAAGGGCAGTCTCTGTCCCGGGCAGGATGGGCC	1377
Db	1362	GACCTCAG---CACCACCAACCACTACCAAGGGCAGTCTCTGTCCCGGGCAGGATGGGCC	1418
Qy	1378	AGCCCAAGTTCAGCTCAGCTACCAATGGGCACCTGCTCAGCCCCCTGGTGGCGGCGGCCAC	1437
Db	1419	AGCCCAAGTTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCCCCCTGGTGGCGGCGGCCAC	1478
Qy	1438	ACACTGCACCACACAGTCTCCCACTCTGAGCGCGAGAGTTCGTCTCCCGCTCTCCACC	1497
Db	1479	ACACTGCACCACAGTCTCCCACTCTGAGCGCGAGAGTTCGTCTCCCGCTCTCCACC	1538
Qy	1498	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACAGCAACATGACCTATGGGACCTTCAAC	1557
Db	1539	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACAGCAACATGACCTATGGGACCTTCAAC	1598
Qy	1558	TTCTCGGGGCGGCTGATGATCCCTTAATACAGGTATCAGCCCTCATCCCCCCAGAT	1617
Db	1599	TTCTCGGGGCGGCTGATGATCCCTTAATACAGGTATCAGCCCTCATCCCCCCAGAT	1658
Qy	1618	GCATATACCCGAGGGAAGTCTATGAGATCTACTCTACGCTGCACAAAGCCGGAAGAGCTG	1677
Db	1659	GCATATACCCGAGGGAAGTCTATGAGATCTACTCTACGCTGCACAAAGCCGGAAGAGCTG	1718
Qy	1678	AGTTGCCCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATGCTTTAGCTGTGAGACCCCT	1737
Db	1719	AGTTGCCCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATGCTTTAGCTGTGAGACCCCT	1778
Qy	1738	GGGCTCTGCTCACCAGGCGGCTCATCTGGCTATGGACCACTGTGGGGAGCCAGCCCT	1797
Db	1779	GGGCTCTGCTCACCAGGCGGCTCATCTGGCTATGGACCACTGTGGGGAGCCAGCCCT	1838
Qy	1798	GACAGCTGGAGCTGCGCCCTCAAAAAGCAGTCCGTGCGAGGGCAGCTGGG---AGGATGTG	1854
Db	1839	GACAGCTGGAGCTGCGCCCTCAAAAAGCAGTCCGTGCGAGGGCAGCTGGGAGAGGATGTG	1898
Qy	1855	CTGCACCTGGGCGAGGAGCGCCCTCCACCTCTACTGTCAGCTGTGAGGCGCAGTGCC	1914
Db	1899	CTGCACCTGGGCGAGGAGCGCCCTCCACCTCTACTGTCAGCTGTGAGGCGCAGTGCC	1958
Qy	1915	TGCTAGCTCTTACCGAGCAGCTGGGCGCTTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	1974
Db	1959	TGCTAGCTCTTACCGAGCAGCTGGGCGCTTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	2018
Qy	1975	GCTGCGCGCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCACTCCCTCGAG	2034
Db	2019	GCTGCGCGCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCACTCCCTCGAG	2078
Qy	2035	TACAAATCCGGGTCTATCGCTGCAATGACACCCCAAGTGCACCTCAAGAGAGTGTGCGAG	2094
Db	2079	TACAAATCCGGGTCTATCGCTGCAATGACACCCCAAGTGCACCTCAAGAGAGTGTGCGAG	2138
Qy	2095	CTGGAGAAGCAGCTGGGGGAGCAGCTGATCCAGAGGCACGGGTCTGTGCACTTCAAGGAC	2154
Db	2139	CTGGAGAAGCAGCTGGGGGAGCAGCTGATCCAGAGGCACGGGTCTGTGCACTTCAAGGAC	2198
Qy	2155	AGTTACCAACCACTGGCCCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG	2214
Db	2199	AGTTACCAACCACTGGCCCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG	2258
Qy	2215	CTCCTTGTGAGCTACAGGAGATCCCTTTTATACATCTGGAATGGCAGCGCGGTAC	2274
Db	2259	CTCCTTGTGAGCTACAGGAGATCCCTTTTATACATCTGGAATGGCAGCGCGGTAC	2318
Qy	2275	TTGCACTGCACCTTACCCCTGGAGCGGTGTGAGCCCCCAGCAGCTAGTGACCTGGGCTGCAAG	2334

Db 2319 TTGCACATGCACCTTCCACCTGAGGGTGTGAGCCCGACCACTAGTGACCTGGCCCTGCAAG 2378
Qy 2335 CTGTGGGTGTGCGAGGTGAGGGCGACGGGCGAGAGCTTCAGCATCAACTTCAACATCACC 2394
Db 2379 CTGTGGGTGTGCGAGGTGAGGGCGACGGGCGAGAGCTTCAGCATCAACTTCAACATCACC 2438
Qy 2395 AAGGACACAAAGTTTGTCTGAGCTGTGGCTCTGAGAGAGTGAAGCGGGGGTCCAGCCCTG 2454
Db 2439 AAGGACACAAAGTTTGTCTGAGCTGTGGCTCTGAGAGAGTGAAGCGGGGGTCCAGCCCTG 2498
Qy 2455 GTGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCGGCGAAGATTAATTTCCAGCCTG 2514
Db 2499 GTGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCGGCGAAGATTAATTTCCAGCCTG 2558
Qy 2515 GACCCACCTGTAGCGGGGTGCGACCTGCGGAGCTGTGGCCCGACCACTCCACTGGAC 2574
Db 2559 GACCCACCTGTAGCGGGGTGCGGACCTGCGGAGCTGTGGCCCGACCACTCCACTGGAC 2618
Qy 2575 AGCCATCTCAGCTCTTTTGGCTTCAAGCCCGAGCCCGACGAGCATGATCCTCAACTGTGG 2634
Db 2619 AGCCATCTCAGCTCTTTTGGCTTCAAGCCCGAGCCCGACGAGCATGATCCTCAACTGTGG 2678
Qy 2635 GAGCGCGGCACTTCCCGCAACGGGCAACCTCAGCCAGCTGGCTGCGAGCATGGCTGGACTG 2694
Db 2679 GAGCGCGGCACTTCCCGCAACGGGCAACCTCAGCCAGCTGGCTGCGAGCATGGCTGGACTG 2738
Qy 2695 GCGCAGCCAGACGCTGGGCTTTCACAGTTCGGAGGCTGAGTCTGAGGCGGCGCCAG 2752
Db 2739 GCGCAGCCAGACGCTGGGCTTTCACAGTTCGGAGGCTGAGTCTGAGGCGGCGCCAG 2796

RESULT 5

ID ADH71609 standard; DNA; 2881 BP.
XX AC ADH71609;
XX AC
XX AC
DT 25-MAR-2004 (first entry)
XX AC
DE Human gene of the invention NOV21a SEQ ID NO:505.
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX OS Homo sapiens.
XX OS
XX PN WO2003102155-A2.
XX PD 11-DEC-2003.
XX PF
XX PF 03-JUN-2002; 2003WO-US017430.
XX PF
XX PF 03-JUN-2002; 2002US-0385120P.
XX PF 04-JUN-2002; 2002US-0385784P.
XX PF 05-JUN-2002; 2002US-0386041P.
XX PF 05-JUN-2002; 2002US-0386047P.
XX PF 06-JUN-2002; 2002US-0386376P.
XX PF 06-JUN-2002; 2002US-0386453P.
XX PF 06-JUN-2002; 2002US-0386864P.
XX PF 06-JUN-2002; 2002US-0387016P.
XX PF 07-JUN-2002; 2002US-0386796P.
XX PF 07-JUN-2002; 2002US-0386816P.
XX PF 07-JUN-2002; 2002US-0386931P.
XX PF 07-JUN-2002; 2002US-0386942P.
XX PF 07-JUN-2002; 2002US-0386971P.
XX PF 07-JUN-2002; 2002US-0387262P.
XX PF 08-JUN-2002; 2002US-0296960P.
XX PF 10-JUN-2002; 2002US-0387400P.
XX PF 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 21-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
PA (CURA-) CURAGEN CORP.
XX PA
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ,
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Etenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS,
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX WPI; 2004-081935/08.
DR

DR	P-PSDB; ADH71610.	
XX		
PT	New NOVX polypeptides and nucleic acid molecules useful for preventing or	
PT	treating NOVX-associated disorders, e.g. cancer, diabetes, infection or	
PT	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.	
XX		
PS	Example 21; SEQ ID NO 505; 1980pp; English.	
XX		
CC	The invention relates to a novel isolated polypeptide (NOVX). A	
CC	polypeptide of the invention has cytostatic, immunomodulator,	
CC	neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and	
CC	antilipase activity, and may have a use in gene therapy, and as a	
CC	vaccine. The polypeptides are encoded by NOVX polynucleotides comprising	
CC	any of the 303 fully defined nucleotide sequences given in the	
CC	specification. The polypeptide is useful in the manufacture of a	
CC	medicament for treating a syndrome associated with a human disease. The	
CC	polypeptide, polynucleotide and antibody are useful in diagnosing,	
CC	treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,	
CC	Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious	
CC	diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are	
CC	further used as hybridisation probes, in chromosome mapping, tissue	
CC	typing, preventive medicine, and pharmacogenomics. The present sequence	
CC	encodes a NOVX polypeptide of the invention.	
XX		
SQ	Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;	
	Query Match 97.3%; Score 2676.4; DB 12; Length 2881;	
	Best Local Similarity 98.9%; Pred. No. 0;	
	Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;	
Qy	1 CCGGGGGCCCGCGCCGCGCCCGCCCTGCGCCGCGCGGCATGGCGCTCGGCCCC	60
Db	42 CCGGGGGCCCGCGCCGCGCCCGCCCTGCGCCGCGCGCATGGCGCTCGGCCCC	101
Qy	61 GGCCTGTGGCCAGCGCTCTGGGCATAGTCTCCCGCTTGGCTCCGCGGCTCGGGTGC	120
Db	102 GGCCTGTGGCCAGCGCTCTGGGCATAGTCTCCCGCTTGGCTCCGCGGCTCGGGTGC	161
Qy	121 CAGCAGAGTGCCACCGTGGCCAAACCCAGTGCTGGTGCCAAACCGGACCTGTTCCCCAC	180
Db	162 CAGCAGAGTGCCACCGTGGCCAAACCCAGTGCTGGTGCCAAACCGGACCTGTTCCCCAC	221
Qy	181 TTCTGTGTGGAGCCGAGGATGTATCATGCTCAAGAACAGCCAGTGCTGTGTGTGC	240
Db	222 TTCTGTGTGGAGCCGAGGATGTATCATGCTCAAGAACAGCCAGTGCTGTGTGTGC	281
Qy	241 AAGCCGTGTCGCGCCAGCAGATCTTCTTCAAGTGCAACCGGGAGTGGTGCGCCAGGTG	300
Db	282 AAGCCGTGTCGCGCCAGCAGATCTTCTTCAAGTGCAACCGGGAGTGGTGCGCCAGGTG	341
Qy	301 GACCAGTGATCGAGCGCAGCAGACGCGGAGCAGTGGGTGCCCAACATGGAGGTCGCG	360
Db	342 GACCAGTGATCGAGCGCAGCAGACGCGGAGCAGTGGTGAGCGGACCATGGAGTCCGC	401
Qy	361 ATTAATGCTCAAGCAGCAGGTGCGAAGGTGTTCCGGCTGGAGGAATCTGGTCCAG	420
Db	402 ATTAATGCTCAAGCAGCAGGTGCGAAGGTGTTCCGGCTGGAGGAATCTGGTCCAG	461
Qy	421 TGCCTGGCATGGAGCTCTCCGGGCACCAAGAGTCAGAAAGGCTCATCCCGCATAGCC	480
Db	462 TGCCTGGCATGGAGCTCTCCGGGCACCAAGAGTCAGAAAGGCTCATCCCGCATAGCC	521
Qy	481 AGATTGGCAAGAACTTCAGCAGAGCGCGCTGGCCAAAGAGGTGTCCCTGGAGCAGGC	540
Db	522 AGATTGGCAAGAACTTCAGCAGAGCGCGCTGGCCAAAGAGGTGTCCCTGGAGCAGGC	581
Qy	541 ATCTGTGCTCCCTCGCTCCACCGGAGGATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	600
Db	582 ATCTGTGCTCCCTCGCTCCACCGGAGGATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	641
Qy	601 AACGAGGACCTGTGGACCCGCTCCCTGGACCCCAATGTATACATCAACGCGGGACAGC	660
Db	642 AACGAGGACCTGTGGACCCGCTCCCTGGACCCCAATGTATACATCAACGCGGGACAGC	701
Qy	661 CTGTGTGTGCGACAGGCCCCCGCTTGTGTGACACGCGCCAACTACACCTCGTGGCGCAAGAAC	720
Db	702 CTGTGTGTGCGACAGGCCCCCGCTTGTGTGACACGCGCCAACTACACCTCGTGGCGCAAGAAC	761
Qy	721 ATGTGTGACGTGCGCGCAGCGCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
Db	762 ATGTGTGACGTGCGCGCAGCGCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	821
Qy	781 TCAGACGTGACCGAGTGGTCCGTCTGTGAGCGCCAGCTGTGTGGCGCGCTGTGGCAAGAACGG	840
Db	822 TCAGACGTGACCGAGTGGTCCGTCTGTGAGCGCCAGCTGTGTGGCGCGCTGTGGCAAGAACGG	881
Qy	841 AGCGGAGCTGACCAACCGCGCGCTCTTCAACGCGGCGCTTCTGTGTGAGGGGCAAGAT	900
Db	882 AGCGGAGCTGACCAACCGCGCGCTCTTCAACGCGGCGCTTCTGTGTGAGGGGCAAGAT	941
Qy	901 GTCCAGAA---AACAGCTGGGCCACCCCTGTGCGCCAGTAGACGCGAGCTGAGGCCGTGG	957
Db	942 GTCCATGACCGCACCGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1001
Qy	958 AGCAAGTGTGCGGCTGTGGGCTGGACTGCAACCCACTGTGGCGGAGCCGTGTGTGTGTGTGT	1017
Db	1002 AGCAAGTGTGCGGCTGTGGGCTGGACTGCAACCCACTGTGGCGGAGCCGTGTGTGTGTGT	1061
Qy	1018 CAGACACCCCGCAAGAGGGGAGGAGTGCCAGGGCACTGACCTGTGACACCCGCAACTGT	1077
Db	1062 CAGACACCCCGCAAGAGGGGAGGAGTGCCAGGGCACTGACCTGTGACACCCGCAACTGT	1121
Qy	1078 ACCAGTGACCTCTGTGTACACAGTGCTTGTGGCCCTGAGGACCTGGCCCTCTATGTGGGC	1137
Db	1122 ACCAGTGACCTCTGTGTACACAGTGCTTGTGGCCCTGAGGACCTGGCCCTCTATGTGGGC	1181
Qy	1138 CTATCGCCGTGGCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1197
Db	1182 CTATCGCCGTGGCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1241
Qy	1198 CGAAGAGAGGAGGGCTGGACTCAGATGTGGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTG	1257
Db	1242 CGAAGAGAGGAGGGCTGGACTCAGATGTGGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTG	1301
Qy	1258 CAGCCGTGAGCTCAAGCCAGCAAGACAGACAAACCCCATCTGCTCACCATCCAGCCG	1317
Db	1302 CAGCCGTGAGCTCAAGCCAGCAAGACAGACAAACCCCATCTGCTCACCATCCAGCCG	1361
Qy	1318 GACTCAGACCAACCAACCACTACAGGGAGTCTCTGTCCCGGAGGATGGGCCC	1377
Db	1362 GACTCAG---CACCACCAACCACTACAGGGAGTCTCTGTCCCGGAGGATGGGCCC	1418
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Db	1419 AGCCCAAGTTCAGCTCAACCAATGGGACCTGCTCAGCCCTGCGGTGGGGCGGCCAC	1478
Qy	1438 ACCTGCAACCAACCACTCTGAGCGCGGAGGTTGCTCTCCGCTCTCCACC	1497
Db	1479 ACCTGCAACCAACCACTCTGAGCGCGGAGGTTGCTCTCCGCTCTCCACC	1538
Qy	1498 CAGAACTACTTCGCTCCCTGCGCCAGGACCAAGCAACATGACCTATAGGACCTTCAAC	1557
Db	1539 CAGAACTACTTCGCTCCCTGCGCCAGGACCAAGCAACATGACCTATAGGACCTTCAAC	1598
Qy	1558 TTCTCTGGGGCGCGGTGATGATCCCTAATACAGGATACGCTCTCTCTCTCTCTCTCTCTCTCT	1617
Db	1599 TTCTCTGGGGCGCGGTGATGATCCCTAATACAGGATACGCTCTCTCTCTCTCTCTCTCTCTCT	1658
Qy	1618 GCATACCCCGAGGAGATCTATGAGATCTACCTCAGCTGCAAGAGCGGAGAGAGCTG	1677
Db	1659 GCATACCCCGAGGAGATCTATGAGATCTACCTCAGCTGCAAGAGCGGAGAGAGCTG	1718
Qy	1678 AGGTGCCCCCTAGCTGGCTGTGACACCTGCTGAGTCCCATCGTTAGCTGTGAGACCCCT	1737
Db	1719 AGGTGCCCCCTAGCTGGCTGTGACACCTGCTGAGTCCCATCGTTAGCTGTGAGACCCCT	1778

Qy 1738 GGCGTCTGCTCAACCGGCCAGTTCATCTGCTGATGACCACTGTGGGGAGCCAGCCCT 1797
Db 1779 GGCGTCTGCTCAACCGGCCAGTTCATCTGCTGATGACCACTGTGGGGAGCCAGCCCT 1838
Qy 1798 GACAGCTGGAGCCTGGCGCTCAAAAGCAGTGTGGAGGCGCAGCTGGG---AGGATGTG 1854
Db 1839 GACAGCTGGAGCCTGGCGCTCAAAAGCAGTGTGGAGGCGCAGCTGGGAGGAGATGTG 1898
Qy 1855 CTGCACTCTGGCGGAGGAGGCGCCCTCCACCTCTACTACTGCGAGCTGGAGGCGCAGTGCC 1914
Db 1899 CTGCACTCTGGCGGAGGAGGCGCCCTCCACCTCTACTACTGCGAGCTGGAGGCGCAGTGCC 1958
Qy 1915 TGCTACGCTTCAACGAGCAGCTGGCGCGCTTTCCCTGTGGAGAGCGCCCTCAGCGTG 1974
Db 1959 TGCTACGCTTCAACGAGCAGCTGGCGCGCTTTCCCTGTGGAGAGCGCCCTCAGCGTG 2018
Qy 1975 GCTGCGCGCAAGCGCCTCAAGCTGCTTCTGTTTGGCGCGGTGGCCTGCACCTCCCTCGAG 2034
Db 2019 GCTGCGCGCAAGCGCCTCAAGCTGCTTCTGTTTGGCGCGGTGGCCTGCACCTCCCTCGAG 2078
Qy 2035 TACAACATCCGGGTCTACTGCTGCTCATGACACCCACGATGCACCTCAAGGAGGTGGTCAG 2094
Db 2079 TACAACATCCGGGTCTACTGCTGCTCATGACACCCACGATGCACCTCAAGGAGGTGGTCAG 2138
Qy 2095 CTGGAGAAAGCAGCTGGGGGAGCAGCTGATCCAGAGCCACGGGTCTCTGCACTTCAAGGAC 2154
Db 2139 CTGGAGAAAGCAGCTGGGGGAGCAGCTGATCCAGAGCCACGGGTCTCTGCACTTCAAGGAC 2198
Qy 2155 AGTTACCAACACCTGGCGCTTCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2214
Db 2199 AGTTACCAACACCTGGCGCTTCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2258
Qy 2215 CTCTCTGTGAGTACACGAGGAGTCCCTTTTATCACAATCTGGAATGCGACGCGGTAC 2274
Db 2259 CTCTCTGTGAGTACACGAGGAGTCCCTTTTATCACAATCTGGAATGCGACGCGGTAC 2318
Qy 2275 TTGCACATGCACTTCAACCTGGAGCGTGTGAGCCCCAGCACTAGTGAACCTGGCGTGAAG 2334
Db 2319 TTGCACATGCACTTCAACCTGGAGCGTGTGAGCCCCAGCACTAGTGAACCTGGCGTGAAG 2378
Qy 2335 CTGTGGGTGTGGAGGTTGGAGGGGAGCGGCGAGCTTTCAGCATCACTTCAACATCACC 2394
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Qy 2395 AAGGACACAAGGTTTGTGAGCTGCTGGCTCTGAGAGTGAAGCGGGGTCCCAAGCCCTG 2454
Db 2439 AAGGACACAAGGTTTGTGAGCTGCTGGCTCTGAGAGTGAAGCGGGGTCCCAAGCCCTG 2498
Qy 2455 GTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCGGCAGAGATAAATTTCCAGCCTG 2514
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Qy 2635 GAGCGCGGCACTTCCCAACGGCAACCTCAGCCAGCTGCTGAGCAGTGGCTGGACTG 2694
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Qy 2695 GGCAGGCGAGCGCTGGCCTCTTCAAGTGTGGAGGCTGAGTGTGAGCGCGGCCAG 2752
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RESULT 6

ADH71649

ID ADH71649 standard; DNA; 2881 BP.

XX

AC ADH71649;
XX DT 25-MAR-2004 (first entry)
XX DE Human gene of the invention NOV21u SEQ ID NO:545.
XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX OS Homo sapiens.
XX PN WO2003102155-A2.
XX PD 11-DEC-2003.
XX PF 03-JUN-2003; 2003WO-US017430.
XX PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
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PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387688P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
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PR 17-JUN-2002; 2002US-0389729P.
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PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402566P.
PR 09-AUG-2002; 2002US-0402589P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403488P.
PR 13-AUG-2002; 2002US-0403531P.

QY 1198 CGAAGAGAGGGGCTGGAATCAGATGTGGTGAATCGTCAATTTCTCACTCAGGCTTC 1257
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Db 1302 CAGCCCGTCAGATCAAGCCGAGCAAGAGAGCAAAACCCCACTGCTCACCATCCAGCG 1361
QY 1318 GACCTCAGCACCACACACACACCTACACAGGCGAGTCTCTCCCGGAGAGATGGGCC 1377
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QY 1855 CTGCACCTGGCGAGGAGGCGCCCTCCCACTCTACTGCTGAGCTGGAGGCGAGTGGC 1914
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Db 2019 GCTGCGCCCAAGCGCTCAAGCTGCTTCTGTTTGGCGGCTGCGCTGACCTCCCTCGAG 2078
QY 2035 TACAACATCCGGGCTACTGCTGATGACACCCAGTGCACCTCAGGAGGTGGTCAG 2094
Db 2079 TACAACATCCGGGCTACTGCTGCTGATGACACCCAGTGCACCTCAGGAGGTGGTCAG 2138
QY 2095 CTGGAAGAGCAGCTGGGGGAGCAGCTGATCAGGAGCCACGGGCTCTGCACTTCAAGGAC 2154
Db 2139 CTGGAAGAGCAGCTGGGGGAGCAGCTGATCAGGAGCCACGGGCTCTGCACTTCAAGGAC 2198
QY 2155 AGTTACCAACACTGCGCTATCATCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2214
Db 2199 AGTTACCAACACTGCGCTATCATCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2258
QY 2215 CTCTTGTGCTACCTACAGGAGATCCCTTTTATCATCTGGAATGCGACCGCGGTAC 2274
Db 2259 CTCTTGTGCTACCTACAGGAGATCCCTTTTATCATCTGGAATGCGACCGCGGTAC 2318

QY 2275 TTGCACTGCACCTTCAACCTGGAGCGTGTGAGCCCGAGCACTAGTGAACCTGGCCTGCAAG 2334
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QY 2335 CTGTGGGTGTGGCAGGTGGAGGCGAGCGGCGAGAGCTTTCAGCATCAACTTCAACATCACC 2394
Db 2379 CTGTGGGTGTGGCAGGTGGAGGCGAGCGGCGAGAGCTTTCAGCATCAACTTCAACATCACC 2438
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Db 2499 GTGGGCCCGAGTGCCTTCAAGATCCCTTCTCATTCGGCAGAAAGATAATTTTCAGCCCTG 2558
QY 2515 GACCCACCTGTAGCGGGGTGCGACTGCGGAGCTCTGGCCCGAGAACTCCACCTGGAC 2574
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QY 2635 GAGCGCGGCACTTCCCAACCGCAACTCAGCCAGCTGGCTGCGAGCTGGCTGGACTG 2694
Db 2679 GAGCGCGGCACTTCCCAACCGCAACTCAGCCAGCTGGCTGCGAGCTGGCTGGACTG 2738
QY 2695 GGCAGCGCAGACGCTGCGCTCTTCAAGTGTGCGAGCTGAGTGTGAGGCGCGGCCAG 2752
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RESULT 7
ADH71635
ID ADH71635 standard; DNA; 2881 BP.
XX AC ADH71635;
XX AC ADH71635;
DT 25-MAR-2004 (first entry)
XX Human gene of the invention NOV21n SEQ ID NO:531.
ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
anorectic; antidiabetic; antimicrobial; antilipase; gene therapy;
vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
obesity; diabetes; infectious disease; metabolic syndrome X;
dyslipidaemia.
XX Homo sapiens.
XX XX
PN W02003102155-A2.
XX 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.

Db 642 AACGAGACCTGGTGGACCCGCTCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 701
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661 CTGGTGGTGGACAGCGCCGCGCTTCTGTGACACGGCCAACTACACTGCTGGTGGCCAAAGAAC 720
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702 CTGGTGGTGGACAGCGCCGCGCTTCTGTGACACGGCCAACTACACTGCTGGTGGCCAAAGAAC 761
Qy
721 ATCTGGGACAGTGGCCGCGAGCGCCCTCCGCTGCTGTCTATCGTCTAAGTGAACGGTGGGTGG 780
Db
762 ATCTGGGACAGTGGCCGCGAGCGCCCTCCGCTGCTGTCTATCGTCTAAGTGAACGGTGGGTGG 821
Qy
781 TCGAGCTGGACGGAGTGGTTCGCTGTGACGCCAGCTGTGGCGCGGTGCGCAGAAACGG 840
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822 TCGAGCTGGACGGAGTGGTTCGCTGTGACGCCAGCTGTGGCGCGGTGCGCAGAAACGG 881
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841 AGCCGGAGCTGCACCAACCCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGAAT 900
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882 AGCCGGAGCTGCACCAACCCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGAAT 941
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901 GTCCAGAA --- AACAGCCTGCGCCACCTGTGTCGCCAGTAGCGGAGCTGGAGCCCGTGG 957
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942 GTCCATGACCGCACCGTCTCTCTCTGTGCTGTGCTGTGAGCGGAGCTGGAGCCCGTGG 1001
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958 AGCAAGTGGTGGCGCTGTGGCTGGACTGTGACCCACTGGCCGAGCGGTGAGTGTCTGAC 1017
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1002 AGCAAGTGGTGGCGCTGTGGCTGTGAGCTGACCTGACCACTGGCGGAGCGGTGAGTGTCTGAC 1061
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1018 CCAGCACCCCGCAACGGAGGGGAGAGTGGCAGGGSCACTGACCTGGACACCCGCAACTGT 1077
Db
1062 CCAGCACCCCGCAACGGAGGGGAGAGTGGCAGGGSCACTGACCTGGACACCCGCAACTGT 1121
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1078 ACCAGTGACCTCTGTGTACACAGTGTCTTCTGGCCCTGAGAGCGTGGCCCTCTATGTGGGC 1137
Db
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Db
1182 CTGATCGCGGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1241
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1198 CGGAAGAGAGGGGCTGAGCTCAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
Db
1242 CGGAAGAGAGGGGCTGAGCTCAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
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1438 ACATGCAACCAAGCTCTCCACCTCTGAGGCCGAGGAGTTGCTCTCCCGCTCTCCACC 1497
Db
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Db
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1558 TTCTCGGGGCGCGCTGATGATCCCTAAATACAGGTATCAGCTTCTATCCCGCCCGAGAT 1617
Db
1599 TTCTCGGGGCGCGCTGATGATCCCTAAATACAGGTATCAGCTTCTATCCCGCCCGAGAT 1658
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1618 GCCATACCCCGAGGGAAGATCTATGAGATCTATCTCAGCTGCAACAGCCCGGAAGAGCTG 1677
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1659 GCCATACCCCGAGGGAAGATCTATGAGATCTATCTCAGCTGCAACAGCCCGGAAGAGCTG 1718
Qy
1678 AGGTTGCCCTTAGCTGGCTGTGACACCCCTGTGAGTCCCATCTGTTAGCTGGACCCCT 1737
Db
1719 AGGTTGCCCTTAGCTGGCTGTGACACCCCTGTGAGTCCCATCTGTTAGCTGGACCCCT 1778

RESULT 8
ADH71637
ID ADH71637 standard; DNA; 2881 BP.

Qy 1738 GGCGTCTGTCTACCCCGGCCAGTCACTCTGTGCTATGGACCACTGTGGGGAGCCCGACCCCT 1797
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1779 GGCGTCTGTCTACCCCGGCCAGTCACTCTGTGCTATGGACCACTGTGGGGAGCCCGACCCCT 1838
Qy 1798 GACAGCTGGAGCTTGCCTCTCAAAAAGACGTCGTGCGAGGGCAGCTGGG --- AGGATGTG 1854
Db
1839 GACAGCTGGAGCTTGCCTCTCAAAAAGACGTCGTGCGAGGGCAGCTGGGAGCAGATGTG 1898
Qy 1855 CTGCACTGGGCGAGGAGGGCGCTCTCCACCTCTACTACTGCGCAGCTGGAGGCCAGTGCC 1914
Db
1899 CTGCACTGGGCGAGGAGGGCGCTCTCCACCTCTACTACTGCGCAGCTGGAGGCCAGTGCC 1958
Qy 1915 TGCTTACGCTCTTACCGAGCAGCTGGCGCTTTCCTCTGTGGGAGAGGCCCTCAGCGTG 1974
Db
1959 TGCTTACATCTTACCGAGCAGCTGGCGCTTTCCTCTGTGGGAGAGGCCCTCAGCGTG 2018
Qy 1975 GCTGCGCCAAAGCGCTCAAGCTGCTTCTGTTTTCGCGGCTGGCTGCGACCTCCCTCGAG 2034
Db
2019 GCTGCGCCAAAGCGCTCAAGCTGCTTCTGTTTTCGCGGCTGGCTGCGACCTCCCTCGAG 2078
Qy 2035 TACAACATCGGGTCTACTGCTGCTGATGACACCCACGATGCACTCAAGGAGGTGGTGCAG 2094
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2079 TACAACATCGGGTCTACTGCTGCTGATGACACCCACGATGCACTCAAGGAGGTGGTGCAG 2138
Qy 2095 CTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCAGCGGCTCTGCACTTCAAGGAC 2154
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2139 CTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCAGCGGCTCTGCACTTCAAGGAC 2198
Qy 2155 AGTTACCAACCTGCGCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2214
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Qy 2275 TTGCACCTGCACTTCACTTGGAGCGTGTGAGCCCGAGCAGCTAGTGTGCTGGCTGCAAG 2334
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2319 TTGCACCTGCACTTCACTTGGAGCGTGTGAGCCCGAGCAGCTAGTGTGCTGGCTGCAAG 2378
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2379 CTGTGGTGTGGCAGGTGGAGGGCGAGCGGCGAGCTTCAAGCATCAACTTCAACATCAC 2438
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2439 AAGGACACAGAGTTTGTGCTGAGCTGCTGCTGAGAGTGAAGGGGGTCCCGAGCCCTG 2498
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2499 GTGGGCGCAGTGTCTTCAAGATCCCTTCTCAATTCGGCAGAGATAAATTTCCAGCCCTG 2558
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2559 GACCCACCTGTAGGCGGGTGGCAGCTGGCGGACTGTGGCCAGAACTCCACCTGAGC 2618
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2679 GAGGCGGGCAGTCTCCCAACCGCAACTCAGCCAGCTGGCTGCGCAGCTGGCTGGAGCTG 2738
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Db
2739 GGCCAGCAGACGCTGGCTCTTTTCAAGTGTGGAGGCTGAGTGTGAGGCGCGCCAG 2796

Db 102 GGCCTGTGGCCAGCGCTCTGGGCATAGTCTGCGCGCTTG3CTCCGCGGCTCG3GTGC 161
Qy 121 CAGCAGATGCCACCGTGGCCAAACCCAGTGCCTGGTGCACACCGGACCTGCTTCCCCAC 180
Db 162 CAGCAGATGCCACCGTGGCCAAACCCAGTGCCTGGTGCACACCGGACCTGCTTCCCCAC 221
Qy 181 TTCTGTGTGGAGCCGAGGATGTGTACATCGTCAAGAACAGCCAGTGTCTTGTGTGC 240
Db 222 TTCTGTGTGGAGCCGAGGATGTGTACATCGTCAAGAACAGCCAGTGTCTTGTGTGC 281
Qy 241 AAGCCGTGTCGCGCCACGACAGATCTTCTCAAGTGCACACCGGGAGTGGTGCACGAGTG 300
Db 282 AAGCCGTGTCGCGCCACGACAGATCTTCTCAAGTGCACACCGGGAGTGGTGCACGAGTG 341
Qy 301 GACCACGTGATCGAGCCGACGACAGCGGAGCAGTGGGCTGCCACCATGGAGGTCCG 360
Db 342 GACCACGTGATCGAGCCGACGACAGCGGAGCAGTGGTGCACCATGGAGGTCCG 401
Qy 361 ATTAATGTCTCAAGCCAGCAGGTGAGAAAGGTGTTGGGCTGGAGGAATACTGTTGCCAG 420
Db 402 ATTAATGTCTCAAGCCAGCAGGTGAGAAAGGTGTTGGGCTGGAGGAATACTGTTGCCAG 461
Qy 421 TGCGTGGATGGAGCTCTCGGGCAACCAAGAGTCAGAAAGCTTACATCCGATAGCC 480
Db 462 TGCGTGGATGGAGCTCTCGGGCAACCAAGAGTCAGAAAGCTTACATCCGATAGCC 521
Qy 481 AGATTGGCAGAACTTCGACAGAGGCGCTGGCCAAAGAGGTGTCCTGGACAGGCG 540
Db 522 AGATTGGCAGAACTTCGACAGAGGCGCTGGCCAAAGAGGTGTCCTGGACAGGCG 581
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Db 822 TCGACGTGGACCGAGTGGTCCGTTGACAGCCAGCTGTGGGCGCGCTG3CAGAAACGG 881
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Db 882 AGCCGGAGCTGCACCAACCGCGCGCTTCAACGGGGCGCTTCTGTGAGGGGCAAGT 941
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Db 1839 GACAGCTGGAGCTGCGCCCTCAAAAAGACGTGCTGCGAGGCGAGCTGGGAGCAGGATGTG 1898
Qy 1855 CTGCACTGGCGGAGGAGCGCCCTCCCACTCTACTACTGCTGAGTGGAGGCGAGTGC 1914
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Qy 1915 TGCTAGCTTTACCGAGCAGCTGGGCGGCTTTGCGCTGTGGAGAGGCGCCCTCAGCGTG 1974
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Qy 1975 GCTGCGCCCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGGCTGCACCTCCCTCGAG 2034
Db 2019 GCTGCGCCCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGGCTGCACCTCCCTCGAG 2078
Qy 2035 TACAACATCCGGGTCTACTGCTGCAATGACCCACGATGCACTCAAGAGGAGTGGTGCAG 2094
Db 2079 TACAACATCCGGGTCTACTGCTGCAATGACCCACGATGCACTCAAGAGGAGTGGTGCAG 2138
Qy 2095 CTGAGAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCAGGGTCTGCACTTCAAGGAC 2154
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Qy 2215 CTCTGTGTAGCTACAGGAGATCCGCTTTTATCAATCTGGAATGGCAACGACGCGTAC 2274
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QY 2335 CTGTGGGTGTGGCAGTGTGGAGGGGAGCGGCGAGAGCTTTCAGCATCAACTTCAACATCAC 2394
DB 2379 CTGTGGGTGTGGCAGTGTGGAGGGGAGCGGCGAGAGCTTTCAGCATCAACTTCAACATCAC 2438
QY 2395 AAGGACACAAGGTTTGTGAGCTGTGCTGTGAGAGTGAAGCGGGGGTCCAGCCCTG 2454
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QY 2455 GTGGGCCCCAGTGCTTCAAGATCCCTTCTCATTCGCGAGAGATAAATTTCCAGCCTG 2514
DB 2499 GTGGGCCCCAGTGCTTCAAGATCCCTTCTCATTCGCGAGAGATAAATTTCCAGCCTG 2558
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QY 2695 GGCAGCGCAGAGCTGGCTTTCACAGTGTGAGAGCTGAGTGTGAGCGGCCAG 2752
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RESULT 9
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ID ADH71641 standard; DNA; 2881 BP.
AC ADH71641;
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XX 25-MAR-2004 (first entry)
XX Human gene of the invention NOV21q SEQ ID NO:537.
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XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyalipidaemia.
XX Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
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XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
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PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;
PI MacLachlan T, Malyankar UM, Mezick AU, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

Db 1719 AGTTGCCCCCTAGCTGGCTGTCTCAGACCCCTGCTGAGTCCCATCGTTAGCTGTGAGACCCCT 1778
Qy 1738 GGCGTCTGTCTCACCAGCCAGTCACTCTGCTATGACCACTGTGTGGGAGCCAGCCCT 1797
Db 1779 GGCGTCTGTCTCACCAGCCAGTCACTCTGCTATGACCACTGTGTGGGAGCCAGCCCT 1838
Qy 1798 GACAGCTGGAGCCTCGCCCTCAAAAGCAGTCTGTCAGAGCCAGCTGGG---AGGATGTG 1854
Db 1839 GACAGCTGGAGCCTCGCCCTCAAAAGCAGTCTGTCAGAGCCAGCTGGGAGCAGATGTG 1898
Qy 1855 CTGACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGACAGCTGGAGCCAGTGCC 1914
Db 1899 CTGACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGACAGCTGGAGCCAGTGCC 1958
Qy 1915 TGCTACTCTTTCACCGAGCAGCTGGGCGCTTTGCTGTTGGGAGAGGCCCTCAGCGTG 1974
Db 1959 TGCTACTCTTTCACCGAGCAGCTGGGCGCTTTGCTGTTGGGAGAGGCCCTCAGCGTG 2018
Qy 1975 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTGGCGCGGTGGCTGCACCTCCCTCGAG 2034
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Qy 2035 TACAACATCCGGGTCTACTGCTCATGACACCCACGATGCACCTCAAGAGAGTGGTGCAG 2094
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Db 2679 GAGCGGGGACTTTCGCCAAGCGGAACTCAGCCAGCTGGTGCAGAGTGGCTGAGCTG 2738
Qy 2695 GGGCAGCAGAGCTGCGCTTCTTCAAGTGTGGAGGCTGAGTCTCAGGCGCGGCCAG 2752
Db 2739 GGGCAGCAGAGCTGCGCTTCTTCAAGTGTGGAGGCTGAGTCTCAGGCGCGGCCAG 2796

ADH71629 standard; DNA; 2881 BP.
ADH71629;
25-MAR-2004 (first entry)
Human gene of the invention NOV21k SEQ ID NO:525.
ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
anorectic; antidiabetic; antimicrobial; antiipamic; gene therapy;
vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
obesity; diabetes; infectious disease; metabolic syndrome X;
dyslipidemia.
Homo sapiens.
WO2003102155-A2.
11-DEC-2003.
03-JUN-2003; 2003WO-US017430.
03-JUN-2002; 2002US-0385120P.
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QY 2635 GAGCGCGGCACTTCCCAAGCGCAACTCAGCCAGCTGGCTGAGCAGTGGCTGGACTG 2694
Db 2679 GAGCGCGGCACTTCCCAAGCGCAACTCAGCCAGCTGGCTGAGCAGTGGCTGGACTG 2738
QY 2695 GCGCAGCCAGAGCTGGCTCTTTCACAGTGTGAGAGTGTGAGTGTGAGGCGCGCCAG 2752
Db 2739 GCGCAGCCAGAGCTGGCTCTTTCACAGTGTGAGAGTGTGAGTGTGAGGCGCGCCAG 2796

RESULT 13

ID ADH71627
XX ADH71627 standard; DNA; 2881 BP.
AC ADH71627;
XX
DT 25-MAR-2004 (first entry)
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DE Human gene of the invention NOV21j SEQ ID NO:523.
XX
KW ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
FN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PP 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
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PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
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PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421566P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;
MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;

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RESULT 2

US-09-306-902A-1
; Sequence 1, Application US/09306902A
; Patent No. 627585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindaay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1

Query Match 82.1%; Score 2259; DB 3; Length 3014;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 2427; Conservative 0; Mismatches 280; Indels 0; Gaps 0;
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QY 646 ACGCGGAGCAGACGCTGTGTGCGACAGCGCCGCTTGTGTGACAGCGGCAACTACACC 705
DB 601 ACGCGGAGCAGACGCTGTGTGCGCTGAGCCCGCTTGGCCGACACGCGCAACTACACC 660
QY 706 TGGTGGCCAAAGAACATCGTGGCAGCGTGGCGAGCGCTCCCGCTGTGTGTATCGTCTAC 765
DB 661 TGTGTGGCCAAAGAACATCGTAGCCCGTGGCGAAGCACCTCTGCGAGGCGCTATTTTAT 720
QY 766 GTGAACGCTGGGTGCTGAGCTGGACCGAGTGTGCTGTGCGAGCGCAGCTGTGGGCGC 825
DB 721 GTGAACGCTGGGTGCTGAGCTGGGTGCTGTGAGTGTGCTGTGAGCGCGCAGCTGTGGGCGT 780
QY 826 GGCTGGCAGAAACGAGCGCGAGCTGACCAACCCCGCGCTCTCTCAACGGGGCGCTTTC 885
DB 781 GGCTGGCAGAAACGAGCGCGAGCTGACCAACCCCGCACCTCTCTCAACGGGGCGCTTTC 840
QY 886 TGTGAGGGGAGAAATGTCCAGAAAAACGCTGGCGCAACCTGTGCGCAGTAGAGCGGAGC 945
DB 841 TGTGAGGGGAGAAATGTCCAGAAAAACAGCCTGGCGCCACTCTGTGCGCCAGTGGGAGC 900

Qy	946	TGGAGCCCGTGGAGCAAGTGTGTGGCTGTGGCTGTGACTGCACCCACTGTGGCGAGCCGT	1005
Db	901	TGGAGTTTGTGGAGTAAGTGTGTGAGCTGTGGCTGTGACTGCACCCACTGTGGCGAGCCGC	960
Qy	1006	GAGTGTCTGTGACCCAGCACCCCGCAACGGAGGGAGGAGTGTCCAGGSCACTGTACTGTGAC	1065
Db	961	GAGTGTCTGTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGGGTGTGTGACCTGTGAC	1020
Qy	1066	ACCCGCAACTGTATACAGTGACTCTGTGTATACAGAGTGTCTTGGCCCTGTAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTATACAGTGACTCTGTGTGTGACACCCGCTTCTTGGCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCTCATGTGGCGTGGCGGTCTGTGCTGTCTGTGTGTCTGTGTGTGTGTGGA	1185
Db	1081	CTCTACATCGGCTTGTGTGCTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGA	1140
Qy	1186	CTCGTTTATTTGCCGGAAGAGGAGGGCTGTGACTCAGATGTGTGGCTGTACTGTGTCCATTCTC	1245
Db	1141	CTCATTTACTTGTGCAAGAAAGAAAGGGCTGTGACTTCOGATGTGGCGGACTGTGTCCATCTC	1200
Qy	1246	ACCTCAGGCTTCCAGGCGGTGTGAGCATCAAGCCAGCAAGAGAGAGAGAGAGAGAGAGAGAG	1305
Db	1201	ACCTCGGGCTTCCAGGCTTGTGAGCATCAAGCCAGCAAGAGAGAGAGAGAGAGAGAGAGAG	1260
Qy	1306	ACCATCCAGCCGAGCTTCCAGCACCAACACCACTTACCAGGCGAGTCTGTGTCCCGG	1365
Db	1261	ACCATCCAGCCGAGACTTCCAGCACCAACCACTTACCAGGCGAGTCTGTGTCCGAGG	1320
Qy	1366	CAGATGTGGCTCCAGCCCAAGTTTCCAGCTTACCAATGGGCACTGTGTCAAGCCCTTGGGT	1425
Db	1321	CAGATGTGACCCAGCCCAAGTTTCCAGCTTCTTAATGGTCACTGTCTCAGCCCACTGGG	1380
Qy	1426	GGCGGCGGCCACACACTGCACCAAGCTCTCCCACTCTGAGGCGGAGGAGTTTGTCTCC	1485
Db	1381	AGTGGCGGCCATAGTTTGACCAAGCTTCCCACTCTGAGGCTGAGGACTTGTGTCTCC	1440
Qy	1486	CGCTCTCCACCCAGAACTACTTCCGCTTCCGTCCGCGGAGGCAACAGCAACATGACCTAT	1545
Db	1441	CGCTCTCCACCCAAACTACTTTCGTTTCCCTGTCCCGGCGCACAGCAACATGGCTTAC	1500
Qy	1546	GGGACCTTCAACTTCTTGGGGGCGGTGTAGTATCCCTTAATCAGATATCAGCTTCTCTC	1605
Db	1501	GGGACCTTCAACTTCTTGGGGGCGGTGTATGTATCCCTTAATCAGGGGATCAGCTTCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCGAGGGAAGATCTACGAGATCTACCTCAGCTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGTTGCCCTAGCTGGCTGTGAGACCTTGTGAGTCCCATCGTTAGC	1725
Db	1621	CCGAGACGTGAGTTTGCCCTAGCTGGCTGTGAGACCTTGTGAGTCCAGTCTGTAGC	1680
Qy	1726	TGTGGACCCCTTGGCGTCTGTCAACCGGCCAGTCAATCTTGGCTATGGAACCATGTGG	1785
Db	1681	TGTGGGCCCCAGGAGTCTGTCAACCGGCCAGTCAATCTTGGCAATGGAACCATGTGGA	1740
Qy	1786	GAGCCAGCCCTGTACAGTGGAGCTGGGCTCAAAAAGCAGTCTGTGCGAGGCGAGCTGG	1845
Db	1741	GAGCCAGCCCTGTACAGTGGAGTCTGGGCTCAAAAAGCAGTCTGTGCGAGGCGAGTGG	1800
Qy	1846	GAGGATGTGTGACCTTGGCGGAGGAGGCGGCTTCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGTGACCTTGGTGAGGAGTCACTTCCACCTCTACTACTTGCAGCTGGAG	1860
Qy	1906	GCCAGTGTGTACTAGTCTTTCACCGAGCACTGGGCGGCTTGTCCCTTGGTGGGAGGCCC	1965
Db	1861	GCCGGGCGCTGTATGTCTTTCACCGAGCAGCTGGGCGGCTTGTCCCTTGTAGGAGGCCC	1920
Qy	1966	CTCAGCTGTGTGGCGGCAAGCGCTCAAGCTGTCTTGTGTGGCGGCTGGCTGCACC	2025
Db	1921	CTCAGCTGTGTGGCGGCAAGCGCTTCAAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT	1980
Qy	2026	TCCCTCGAGTACAACTACCGGGTCTACTGTCTGATGACACCCACAGATGACATCAAGGAG	2085

1981	Db	 TCCCTTGAGTACAAACATCCGAGTGTACTGCTCTACAGACACCCACGACGCTCTCAAGGAG	2040
2086	Qy	GTGCTGCAGCTTGAGAAAGCAGCTGGGGGACAGCTGATCCAGAGGCCACGGGTCCCTGSCAC	2145
2041	Db	GTGCTGCAGCTTGAGAAAGCAGCTAGTGGAGCACTGATCCAGAGCCTCGCTCTCTGCAC	2100
2146	Qy	TTCAAGGACAGTTTACCAAACTTGCCTATCCATCCAGATGCCCAGCTCCCTGTGG	2205
2101	Db	TTCAAGGACAGTTTACCAAACTTGCCTATCCATCCAGAGCTGCCAGCTCCCTGTGG	2160
2206	Qy	AAGAGTAAGCTCTTGTACGCTACGAGAGATCCCTTTTATCACAATCTGGATGSCACG	2265
2161	Db	AAGAGCAAGCTACTTGTACGCTACGAGAGATCCCTTTTATCACAATCTGGAGCGCAC	2220
2266	Qy	CAGCGGTACTTGCATGCGACCTTCACTTGGAGCGTGTAGCCCCCAGCACTAGTGACCTG	2325
2221	Db	CAGCAGTATCTGCATGCGACCTTCACTTGGAGCGCATCAACGCCAGCACCGGACCTG	2280
2326	Qy	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGCGAGCTTTCAGATCAAACTTC	2385
2281	Db	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGAGATGGGCAGAGCTTCAACATCAAACTTC	2340
2386	Qy	AACATCAACAAGGACACAAAGTTTTGTAGCTGCTGCTCTGAGAGTGAAGCGGGGTC	2445
2341	Db	AACATCACTAAGGACACAAAGTTTGTGTAATTTGTGGCTCTGGAGAGTGAAGGGGGGTC	2400
2446	Qy	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTCGGCAGAGAATAAT	2505
2401	Db	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTCGGCAAAAAGATCATC	2460
2506	Qy	TCAGCCTTGACCCACCGCTGTAGCGGGGTGCCGACTGCGGAGACTGTGGCCCAAGAACTC	2565
2461	Db	GCCAGTCTGAGCCACCGCTGTAGCGGGGGCGGACTGGAGAACTCTAGCCCAAGAACTT	2520
2566	Qy	CACCTGGACAGCCATCTCAGCTTCTTTTGGCTCTCAAAGCCAGCCGCCACAGCCATGATCCTC	2625
2521	Db	CACCTGGACAGCCATCTTAGCTTCTTTTGGCTCTCAAAGCCAGCCCTACAGCCATGATCCTC	2580
2626	Qy	AACTGTGGAGGCGGGGCACTTCCCAACAGGCAACTCAGCCAGCTGCGTGCAGCAGTG	2685
2581	Db	AACTTATGGGAGGCAAGGCACTTCCCAACAGGCAACTCAGCCAGCTGCGCAGCAGCTGTG	2640
2686	Qy	GCTTGGACTGGGCCAGCCAGACGCTGCGCTCTTCAACAGTGTGCGAGGCTGAGTCTCAGGC	2745
2641	Db	GCGGCACTGGGCCAAACAGATGTGCGCTCTTCAACGCTGTGCGAGGCGGAGTGTGAGAC	2700
2746	Qy	CGGCCAG	2752
2701	Db	CAGCCAG	2707

RESULT 3
 US-08-808-982-2
 : Sequence 2, Application US/08808982
 : Patent No. 5939271
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Tessier-Lavigne, Marc
 : APPLICANT: Leonardo, E. David
 : APPLICANT: Hink, Lindsay
 : APPLICANT: Masu, Masayuki
 : APPLICANT: Kazuko, Keino-Masu
 : TITLE OF INVENTION: Netrin Receptors
 : NUMBER OF SEQUENCES: 8
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSSEE: SCIENCE & TECHNOLOGY LAW GROUP
 : STREET: 268 BUSH STREET, SUITE 3200
 : CITY: SAN FRANCISCO
 : STATE: CALIFORNIA
 : COUNTRY: USA
 : ZIP: 94104
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1787 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-808-982-2

Query Match 56.8%; Score 1562.4; DB 2; Length 1787;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1661; Conservative 0; Mismatches 16; Indels 9; Gaps 8;

QY	1070	GCAACTGTACAGTACCTCTGTGTACACAGTGTCTTGGCCCTGAGAGCGTGCCTCT	1129
DB	1	GCAACTGTACAGTACCTCTGTG-GTACACATGTCTTGGCCCTGAGAGCGTGCCTCT	59
QY	1130	ATGTGGGCTCATCGCCGTGGCGCTGTCTGCTGTCTGCTGTCTGTCTGTCTGTCTGT	1189
DB	60	ATGTGGGCTCATCGCCGTGGCGCTGTCTGCTGTCTGCTGTCTGTCTGTCTGTCTGT	119
QY	1190	TTTATTGCGGAAGAGAGGGGTGGACTCAGATGTGGTGTGATCTGCTCCATTCTCACT	1249
DB	120	TTTATTGCGGAAGAGAGGGGTGGACTCAGATGTGGTGTGATCTGCTCCATTCTCACT	179
QY	1250	CAGCTTCCAGCCGTGAGCATC-ARGCCAGCAAGAGAGCAACCCCATCTGCTCACC	1308
DB	180	CAGCTTCCAGCCGTGAGCATCTAAGCCAGCAAGAGAGCAACCCCATCTGCTCACC	239
QY	1309	ATCCAGCGGACCTCAGACCAACACACACACACACACACACACACACACACACAC	1368
DB	240	ATCCAGCGGACCTCAGACCAACACACACACACACACACACACACACACACACAC	299
QY	1369	GATGGGCCAGCCCAAGTTCCAGTCAACCAATGGGCACTGTCTCAGCCCTCTGGTGGC	1428
DB	300	GATGGGCCAGCCCAAGTTCCAGTCAACCAATGGGCACTGTCTCAGCCCTCTGGTGGC	359
QY	1429	GGCCGCCACACATGCCACACAGCTCTCCACCTCTGAGGCGGAGGATTCGTCTCCGC	1488
DB	360	GGCCGCCACACATGCCACACAGCTCTCCACCTCTGAGGCGGAGGATTCGTCTCCGC	419
QY	1489	CTCTCCACCCAGAACTACTTCCGCTCCCTGCGCCGAGGACACAGCAATGACCTATGGG	1548
DB	420	CTCTCCACCCAGAACTACTTCCGCTCCCTGCGCCGAGGACACAGCAATGACCTATGGG	479
QY	1549	ACCTTCAACTTCTCTGGGGGCGGTGATGATATCCCTAATAAGTATCAGGCTCTCATC	1608
DB	480	ACCTTCAACTTCTCTGGGGGCGGTGATGATATCCCTAATAAGTATCAGGCTCTCATC	539
QY	1609	CCCCCAGATGCATACCCCGAGGAGATCTATGATGATCTACCTCAGCTGCACAGCCG	1668
DB	540	CCCCCAGATGCATACCCCGAGGAGATCTATGATGATCTACCTCAGCTGCACAGCCG	599
QY	1669	GAAAGCTGAGGTTCCTTGGCTGTGCTGCTCAGACCTCTGCTGCTGCTGCTGCTGCTG	1728
DB	600	GAAAGCTGAGGTTCCTTGGCTGTGCTGCTCAGACCTCTGCTGCTGCTGCTGCTGCTG	659
QY	1729	GGACCCCTGCGCTCTGCTCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1788

Qy 2569 CTGACAGCCATCTCAGCTTCTTTGGCTTCCAAAGCCAGCCCAAGCCAGCCATGATCCTCAAC 2628
Db |||||
Qy 1495 CTGACAGCCATCTCAGCTTCTTTGGCTTCCAAAGCCAGCCCAAGCCAGCCATGATCCTCAAC 1554
Db |||||
Qy 2629 CTGTGGAGGCGCGGCACTTCCCAAGCCCAAGCCCAAGCCAGCCAGCTGGCTGACAGTGGCT 2688
Db |||||
Qy 1555 CTGTGGAGGCGCGGCACTTCCCAAGCCCAAGCCCAAGCCAGCTGGCTGACAGTGGCT 1614
Db |||||
Qy 2689 GGACTGGCCAGCCAGACGCTGGGCTC-TTCACAGTG-TGGAGGCTGAGTGGCTGAGGCC 2746
Db |||||
Qy 1615 GGGACTGGCCAGCAGGACGGTGGCTTCTTTACAGTGTGGAGGCTGAGTGGCTGAGGCC 1674
Db |||||
Qy 2747 GGCCAG 2752
Db |||||
Qy 1675 GGCCAG 1680
Db |||||

RESULT 5
US-08-808-982-3
; Sequence 3, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-808-982-3

Query Match 30.6%; Score 841.4; DB 2; Length 2831;
Best Local Similarity 60.0%; Pred. No. 1.3e-178;
Matches 1638; Conservative 0; Mismatches 961; Indels 130; Gaps 9;

Qy 143 ACCAGTGCCTGTGGTCCAAACCCGACCTGCTTCCCACTTCTGTGGTGGAGCCCGAGGATG 202
Db |||||
Qy 104 ACTCTTCCCATCAGACCCCGGAGCAGCTGCTCTCTCTCTCTGTAACACAGAGATG 163
Db |||||
Qy 203 TGATCATGTGCAAGAACAGCAGTGTGCTGTGTGTGCAAGGCGGTGCCCGCCACGAGCA 262
Db |||||
Qy 164 CCTACATCGTAAAGAACAGCCAGTGGAAATTGCACTGCCAGGCGCTTCCCTGCCACACAGA 223
Db |||||

Qy 263 TCTTCTTCAAGTGCACCGGGAGTGGGTGCGCCAGGTGGACCCAGCTGATCGAGCGCAGCA 322
Db |||||
Qy 224 TCTACTTCAAGTGTATAGCGAGTGGGTAGCCAGAAAGCCACGTCACGAGAGAGCC 283
Db |||||
Qy 323 CAGACGGGAGCAGTGGGCTGCCCAACATGGAGGTCCGCATTAAATGTCTCAAGGCGAGG 382
Db |||||
Qy 284 TGGATGAGGCCACAGGCTTCGGAATACGAGAGGTGCAGATAGAGGTGTCTCGGCGAGCAGG 343
Db |||||
Qy 383 TCAGAAAGGTGTTCGGGCTGGAGGAATACTGGTTCGCCAGTCCGCTGGGATGAGAGTCTCTCGG 442
Db |||||
Qy 344 TGGAGGAACCTTTTGGGCTCGAGGACTACTGGTGTCTCAGTGGTGGGCTGGAGTCTTTCGG 403
Db |||||
Qy 443 GCACCAACAGAGTCAAGAGGCTTACATCCGCAATAGCCAGATTGCGCAAGAACTTTCGAGC 502
Db |||||
Qy 404 GAACCAACAGAGTTCGCCGAGCTTACATCCGCAATAGCCAGATTGCGCAAGAACTTTCGAGC 463
Db |||||
Qy 503 AGGAGCGGTGGCCAAAGGAGGTTCCTCGGAGCAGGCAATCGTGTGCTGCCCTGCGGCTCCAC 562
Db |||||
Qy 464 AGGAGCTCTGGCGAAGGAGGTACCTTGGATCATGAGGTCTTCTGCACTGCGCGCCAC 523
Db |||||
Qy 563 CGGAGGGCATCCCTCCAGCGGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCGGT 622
Db |||||
Qy 524 CAGAGGGAGTGCCTGTGGCTGAGGTGGAAATGGCTCAAGAAATGAAGATGTCTCATGATCCG 583
Db |||||
Qy 623 CCTGGACCCCAATGTATATACATCACCGGGAGCACAGCCTGGTGGTGGCAGAGCCCGCC 682
Db |||||
Qy 584 CTGAGGACATACTTCTCTGCTCACCATTTGACCAACCTCATCATCCGCGAGGCGGCC 643
Db |||||
Qy 683 TTGCTGACACGGCCAACTACACCTGGTGGCCAAAGAAATCGTGGGCACTGCGCGCAGCG 742
Db |||||
Qy 644 TCTCAGACACAGCCAACTACACCTGTGTGCGCAAGAAATATTGTGGCCCAAGCGCGGAGCA 703
Db |||||
Qy 743 CTTCCGCTGTCTCATGCTGTACGTGAAACGTTGGTGGTGGTGCAGCTGGACCGAGTGGTCCG 802
Db |||||
Qy 704 CGACGGCCACAGTCATGCTGTATGTGAACGGAGGTGGTCCAGCTGGGCGAAGATGGGTCCAC 763
Db |||||
Qy 803 TCTGACAGCGCCAGCTGTGGCGCGGCTGGCAGAAACGGAGCCGAGCTGCACCAACCCGG 862
Db |||||
Qy 764 CTGTCTCTAACCGCTGGCGCGGAGGTGGCAGAAACGTAAGTACTGACCAACCCAG 823
Db |||||
Qy 863 CGCTCTCAACCGGGCGCTTTCTGTGAGGGGAGAAATGTCCAGAAACAGCCTGCGCCCA 922
Db |||||
Qy 824 CCCCACCTCAATGAGGCTGCTTCTGCGAGGAGCAGGCTTGCAGAGAGACGGCTTGCACCA 883
Db |||||
Qy 923 CCTGTGCCAGTAGACGCGCAGCTGGAGCCCGTGGAGCAGTGGTGGGCTGGGCTGG 982
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Qy 884 CGTGTGCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGGTCCGCTGCAGCAG 943
Db |||||
Qy 983 ACTGCACCCACTGGCGGAGCGGTGAGTGTCTTGCACCCAGCACCCCGCAAGCGGAGGAGG 1042
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Qy 944 AGTGTGGCACTGGCGCAGCGCGAGTGCATGCGACCGCGGCCCGAGAACGGAGGCGGTG 1003
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Qy 1043 AGTGCAGGGCACTGACCTGGACACCCCGCAACTGTACCAAGTACCTCTGTGTACACAGTG 1102
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Qy 1004 ACTGCAGCGGACGCTTACTTGAATCTCAAGAACTGCACCGATGGCTGTGCGTGTGAATC 1063
Db |||||
Qy 1103 CTTCTGGCC-----CTGAGGAGTGGCCCTCT 1129
Db |||||
Qy 1064 AGAGAACTCTAAACGACCCCTAAAGCGCGCCCTGGAGCGCTCGGGAGACGTGGCGCTGT 1123
Db |||||
Qy 1130 ATGTGGGCTC---ATCGCGCGTGGCGCTGTGCTGGTCTGCTGTGCTGTGCTGTCTCATCC 1186
Db |||||
Qy 1124 ATGCGGCGCTCGTGGTGGCGCTTTTGTGGTCTTGGCAGTTCTCATGGCTGTAGGAGTGA 1183
Db |||||
Qy 1187 TCGTTTATTTCGCGAAGAAAGGAGGGCTGGACTCAGATGTGGTGTGACTGTGTCCATT---C 1243
Db |||||
Qy 1184 TCGTGTACCGGAGAAATCGCGGGAATTCGACACGAGACATCACTGACTCTCTGTGTCGCC 1243
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Qy 1244 TCACTCAGGCTTCAGCGCGGTGAGCATCAAGCCAGCAAGCAGACACACCCCATCTGC 1303
Db |||||
Qy 1244 TCACTGTGTGTTCACACCCCGCTCAACTTCAAGACTCAAGAGCCCGCAGCAACCCACAGCTCC 1303
Db |||||

QY 1304 T-----CACCATCCAGCGGACCTCAGACCAACCAACCACTACAGGGAGTCTCT 1357
Db 1304 TGCACCCATCGGCCCTCCGAGCACTAAACGCGAGTGTGGCATCTACCGGAGCCTGTGT 1363
QY 1358 GTCCCGGGCAGGA-----TG 1372
Db 1364 ATGCCCTGCAAGGACTGCGGCAAGATCCCTATGACTAATTCACCCCTTCTGGATCCCT 1423
QY 1373 GGCCAGCCCCAAGTTCAGCTACCAATGGGCACTGTCTCAGCCC-----CTGG 1423
Db 1424 TGCCAGGCTCAAGATCAAGGTCTATGACTCCAGCAACATCGGCTCTGGGCTGGCCTGG 1483
QY 1424 GTGGCGGCGGCAACACTGACACAGCTCTCCCACTCTGAGGCGGAGGTTCTCT 1483
Db 1484 CTGATGAGCGGACCTCTGGGTGTCTTACACCGGTATATACCCAGGGGATTTCTCC 1543
QY 1484 CCGCCTCTCACCCAGAAC-----TACTTCGGCTCCC 1516
Db 1544 GGGACACCACTTCTGCACTGCGCAGCGCAGCCTTGGTCCAGCACTCTCGGGCC 1603
QY 1517 TGCCCGAGGACACAGCAACATGACCTATGGGACCTTCAACTTCTCGGGGCGCGGTGA 1576
Db 1604 TCCCTCGAGACCCCGAGCAGAGTGTCAAGTGGCACCTTTGGTGGCTGGGTGGGAGGCTGA 1663
QY 1577 TGATCCCTAATACAGGTATCAGCTCTCTCATCCCCCAGATGCCATACCCGAGGAGGA 1636
Db 1664 CCAFTCCCGGACAGGGGTGAGCCTGTGTGTTACCAATGAGGCCATTTCCCGAGGGCAAGT 1723
QY 1637 TCTATGAGATCTACTCTCAGCTGACCAAGCGGAGAGACGTGAGGTTCGCCCTAGCTGGCT 1696
Db 1724 TCTATGACTTGTATCTAGCTATCAACAGAGACTGAAAGCACTTCCGAGGTT 1783
QY 1697 GTCAGACCTGTGAGTCCCATGTTAGCTGTGACCCCTGGCGTCTGTCTACCCGCG 1756
Db 1784 CCCAGACAGTATTGAGCCCCCTCGGTGACCTCGGGCCACAGGGCTCTCTCTGTGCGGCC 1843
QY 1757 CAGTCATCCTGGCTATGAGCACTGTGGGAGCCAGCCCTGACAGCTGGAGCTGGGCC 1816
Db 1844 CTGTTGTCTCTACTGTGCCCACTGTGCTGAAGTCAATTGGCGGAGACTGATCTTCAGC 1903
QY 1817 TCAAAAAGCAATCTGCGGAGGCGAGCTGGGAGGATGTCTGACCTGGGCGAGGAGCGC 1876
Db 1904 TCAAGACCCAGGCCCATCAGGCCACTTGGGAGGAGTGTGACTTTGATGAGGAGCTC 1963
QY 1877 CTTCCCACTCTACTACGAGCTGAGGCGAGTGTCTGTGTAAGTCTTACCGAGCAGC 1936
Db 1964 TGAACACCCCTGTACTGCGAGCTAGAGGCTAAATCTGCACTCTGTGAGCAGC 2023
QY 1937 TGGGCGCTTTGCGCTGGGAGAGGCCCTCAGCGTGGCTGCGGCAAGCGCTCAAGC 1996
Db 2024 TGGGTACTAGTGTTCAGGGGAGGCTTACTTCCCGCTCGAGTCAAGCGGCTCAGC 2083
QY 1997 TGCTTCTGTTTGGCGCGGTGGCTGCACTCCCTCGAGTACAAATCCGGGTCTACTGCC 2056
Db 2084 TAGCCATCTTTCGCCCCAGCCCTCTGCACCTCCCTGGAGTATAGTCTCAGGGTCTACTGTC 2143
QY 2057 TGCATGACACCAAGATGCACTCAAGAGGTGTGCACTGGAGAACAGCAGCTGGGGGAG 2116
Db 2144 TGGAGGACACTCTCTGACGACTGAAGGAGTCTTAGAGCTGGAGGAGCTCTGGGTGGCT 2203
QY 2117 AGCTGATCCAGGACGCGGTCTGCACTTCAAGGACAGTTACCAACCTCGGCTAT 2176
Db 2204 ACTTGGTGGAGAGGCCAAGACTTGTCTTTTAAAGACAGTTTACCAACTAGCTAGCTCT 2262
QY 2177 CCATCCAGATGTGCCAGCTCCCTGTGGAAGATAAGCTCTTGTGAGCTACAGGAGA 2236
Db 2263 CCCTCCATGACATCCCCCATGTGCCACTGGAGGACAAACTACTTGGCCAACTACAGGAGA 2322
QY 2237 TCCCTTTTATACATCTGGAATGGCAGCAGCGGTACTTGCATGCACTTACCCCTGG 2296
Db 2323 TTCCCTTTTACATGTGTGGAACGGCAGCCAGAAAGCCCTGCACTGCACTTACCCCTGG 2382
QY 2297 AGCGTGTGAGCCCCAGCACTAGTGAACCTGGGCTGCAAGCTGTGGGTGTGGCAGGTGAGG 2356

Db 2383 AGAGACATAGCCTAGCCTCCACTGAGTTACCTGTAAAGTCTGCTGCGCAGGTAGAAG 2442
QY 2357 GCACGGGAGAGCTTCAAGCATCAACTTCAACATCAC---CAAGGACACAAGGTTTGTCTG 2413
Db 2443 GGGAGGCCAGATTTTCCAGCTGACACACAGCTGGCTGAGAGCGCTGCTCCCTGG 2502
QY 2414 AGCTGTGGCTCTGGAGAGTGAAGCGGGGTCCAGCCCTGTGGGGCCCACTGTAGCGGG 2533
Db 2503 ATGCACTCTGCTCTGCGCCCTGGCAATGCTGCCACCAACACAGCTGGGACCCCTATGCTTCA 2562
QY 2474 AGATCCCTCTCTCATTCGGCAGAGATAATTTTCAGGCTGGACCCCACTGTAGCGGG 2533
Db 2563 AGATAACACTGTCTCCGCGCAGAGATCTGCAACAGCTGGACGCGCCCACTCAGCGG 2622
QY 2534 GTGCCAGCTGGCGGACTCTGGCCCAAGAACTCACTGTGACAGCCATCTCAGCTTCTTTG 2593
Db 2623 GCAATGACTGGCGGCTTGGCACAGAGCTCTCCATGGACCGGTACTTGAATCTCTCG 2682
QY 2594 CTTCAGAGCCAGCCCAAGCCATGATTCCTCAACTGTGGGAGGCGGCGACTTCCCCA 2653
Db 2683 CCACCAAGCTAGTCCACAGGCGTGTATCTTAGACCTCTGGGAAGCTCGGCGAGGATG 2742
QY 2654 ACCGCAACCTCAGCCAGCTGGCTGCGAGCTGGCTGAGTGGCTGGGCGCAGCAGCTGGCC 2713
Db 2743 ATGGGACCTCAACAGCTGGCCAGCTGCTTGGAGGAGATGGGCAAGATGAGATGCTGG 2802
QY 2714 TCTTCAGCTGTCGGAGGCTGAGTGTGTA 2742
Db 2803 TAGCCATGACCACTGATGGCGATTGCTGA 2831

RESULT 6

US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA			
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:			
US-09-306-902A-3			
Query Match 30.6%; Score 841.4; DB 3; Length 2831;			
Best Local Similarity 60.0%; Pred. No. 1.3e-178;			
Matches 1638; Conservative 0; Mismatches 961; Indels 130; Gaps 9;			
Qy	143	ACCAGTGGCTGGTGCACACCGGACCTGCTTCCCACTTCTCTGCTGGAGCCCGAGGATG	202
Db	104	ACTCTTCCCATACGACCCCGGAGCAGCTGCTCTCTCTCTGCTGGAACGAGGATG	163
Qy	203	TGTATCATGTCAGAAACAGCAGCTGCTGCTTGTGTCAAGSCCGTGCCGCCACGAGCA	262
Db	164	CCTACATCGTAAAGAAACAAGCAGTGGAAATGGCACTGCCGAGCCTTCCCTGCCACACAGA	223
Qy	263	TCCTTCTTCAAGTGCAACGGGAGTGGGTGCCGACGTGGACCACTGATCGAGCGCAGCA	322
Db	224	TCTACTTCAAGTGTAAATGGCCAGTGGGTTAGCCAGAAAGGCCACGTCAAGCAGGAGCC	283
Qy	323	CAGACGGGAGCAGTGGGCTGCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG	382
Db	284	TGGATGAGGCCACAGGCTTGGCAATACAGAGGTGCGATGAGGTGTCCGGGAGCAGG	343
Qy	383	TCGAGAAAGGTGTTCCGGCTGGAGGAATACTGGTGCAGTGGCTGGCATGGAGCTCTCTCGG	442
Db	344	TGGAGGAACCTTTTGGGCTCGAGGACTACTGGTGTGCTAGTGGCTGGGCTCTTCGG	403
Qy	443	GCACCAACAGATCAGAAAGCCTACATCCGCATAGCCAGATTTGGGCAAGAACTTCGAGC	502
Db	404	GAACCAACAGATTCGCGAGCCTACATCCGCATTCGCTACTTTCGCAAGAACTTTGACC	463
Qy	503	AGGAGCGCTGGCCCAAGAGGTGTCCTGGAGCAGGCACTGCTGCCCTGCCGCTCCAC	562
Db	464	AGGAGCTCTGGCAAGAGGATACCTTTGGATCATGAGGTCTTCTGAGTGGCCGCCAC	523
Qy	563	CGGAGGGCATCCCTCCAGCCGAGTGGAGTGGCTCCGGAACAGAGCACTGGTGACCCGT	622
Db	524	CAGAGGGAGTGCCCTGTGGCTGAGGTGGAATGGCTCAAGATGGAATGTCAATCCCG	583
Qy	623	CCCTGGACCCCAATGTATATACACGCGGGAGCAAGCCTGGTGGTGGAGCCGCGCC	682
Db	584	CTCAGGACACTAACTTCTCTGCTCAACCATTTGACCAACAACCTCATCCGCGAGCGGCC	643
Qy	683	TTGCTGACAGCGGCCAACTACACCTGCTGGCCCAAGAACATCGTGGCACGCTCGCGCAGCG	742
Db	644	TCTCAGACACAGCCAACTACACCTGTGTGGCAAGAAATATTTGGCCAAAGCCGCGAGCA	703
Qy	743	CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGTGGTGCAGTGGACCGAGTGGTCCG	802
Db	704	CGACGGCCACAGTCAATCGTCTATGTGAACGGAGTTGGTCCAGCTGGGCAAGATGGTCA	763
Qy	803	TCCTGACGGCCAGTGTGGGGCGGCTGGCGAAGAACCGAGCCCGAGCTGCAACCCCG	862
Db	764	CCTGCTCTAAACCGCTGGCGCGAGTTGGCAGAAACGTAAGTGGACCTGCAACCAACCCAG	823
Qy	863	CGCTCTCAACGGGGCGCTTTCTGTCAGGGGCAAGATGTCAGAAACAGCCTTGGCCCA	922
Db	824	CCCACTCAATGAGGTGCTTCTGCGAGGACAGGGCTTGCAGAAACGGCTTTGCACCA	883
Qy	923	CCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGACCAAGTGGTCCGCCCTGTGGGCTGG	982
Db	884	CCGTGTGCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGGTCCGCCCTGCAGCACAG	943
Qy	983	ACTGCAACCACTGGCGGAGCGGTGAGTGTCTGTGACCCAGCAACCCCGCAACGAGAGGAGG	1042
Db	944	AGTGTGGGCACTGGCGCAGCGCGAGTGCATGGCAACCGCGGCCCCAGAACGAGGCGCGTG	1003
Qy	1043	AGTSCCAGGCACTGACTGGACACCGCACTGTACAGTACCTGTGTGTACAGTGT	1102
Db	1004	ACTGACGGGACGCTACTTTGACTTCCAGAACTGCACCGATGGGCTGTGGTGTGAATC	1063
Qy	1103	CTTCTGGCC-----CTGAGGAGGTGGCCCTCT	1129
Db	1064	AGAGAACTCTAAAGCAGCCCTAAAGCCGCCCTTGGAGCGCTCGGAGAGCGTGGCGCTGT	1123
Qy	1130	ATGTGGGCTC-----ATGCGCGTGGCGCTCTGCTGCTGCTGCTGCTGCTCTCTATCC	1186
Db	1124	ATGCGGCTCTGCTGGTGGCGCTCTTTGTGGTTCTTGGCAGTTCTCATGGCTGTAGGAGTGA	1183
Qy	1187	TCGTTTATTCCCGGAAGAGGCGCTGAGCTCAGATGTGGCTGAGTCTGTCATT---C	1243
Db	1184	TCGTGTAACGAGAAACTGCGGGAATTGACACGGAATCATCTGATCTCTCTCTGCTGCC	1243
Qy	1244	TCACCTCAGGCTTTCAGCCCGTCAAGCTCAAGCCAGCAAGAGAGCAACCCCATCTGC	1303
Db	1244	TCACCTGCTGCTTCCACCCCGTCAACTTCAAGACTGCAAGGCCAGCAACCCACAGCTCC	1303
Qy	1304	T-----CACCATTCAGCCGGACTCAGACCAACCAACCACTTACAGGGCAGTCTCT	1357
Db	1304	TGCACCCATCCGCCCTTCGGGACCTTAACGGCCAGTGTGTCATCTACCGGAGCTGTGT	1363
Qy	1358	GTCCCGGCGAGGA-----TG	1372
Db	1364	ATGCCCTGAGGACTCTGCCGACAAGATCCCTATGACTAATTCACCCCTTCTGATCCCT	1423
Qy	1373	GGCCAGCCCAAGTTTCAGCTCAACCAATGGGCACTGTCTCAGCCC-----CCTGG	1423
Db	1424	TGCCAGCCTCAAGATCAAGGTCTATGACTCCAGCACTATCGGCTCTGGGCTGGCCTGG	1483
Qy	1424	GTGGGCGCGCCACACACTGCAACACAGCTCTCCCACTCTGAGGCCGAGAGTTCGTCT	1483
Db	1484	CTGATGGAGCGCAGCTGCTGGGTGCTTTACACCGCGTACATACCCAGGGGATTTCTCCC	1543
Qy	1484	CCGCGCTCTCACCCAGAAC-----TACTTCGCTCCC	1516
Db	1544	GGACACCCACTTCTGCACTCGCGAGCCGAGCCTTGGTTCCAGCACTCTCTGGGCC	1603
Qy	1517	TGCCCGGAGCACAGCAACATGACCTATGGGACCTTCAACTTCTCGGGGCGCGCTGA	1576
Db	1604	TCCTCGAGACCCACAGCAGGTGTCAGTGGCACTTTGGTTGCTGGTGGGAGGCTGA	1663
Qy	1577	TGATCCCTAATACAGGTATCAGGCTCTCTATCCCGCCAGATGCCATACCCGAGGGAAGA	1636
Db	1664	CCATTCGCGCACAGGGGTGAGCCTGTTGGTACAAATGGAGCAATTTCCCGAGGCAAGT	1723
Qy	1637	TCTATGAGATCTACTCAGCTGCACAGCCGGAAGACGTGAGTTGSCCTCTAGCTGCT	1696
Db	1724	TCTATGACTTGTATCTACGTATCAACAGACTGAAGACCCCTCCCACTTTTGGAAAGTT	1783
Qy	1697	GTGAGACCTCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGCGCTCTCTCAACCCGC	1756
Db	1784	CCAGACAGTATTGAGCCCTCGCTGACCTGCGGGCCCAAGGGCTCTCTCTGTGCGGCC	1843
Qy	1757	CAGTCACTCTGGCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGAGGCTGGGCC	1816
Db	1844	CTGTTGCTCTACTGTGCCCCACTGTGCTGAACTCATTTGCGGAGACTGGATCTTCAGC	1903
Qy	1817	TCAAAAGCAGTGTGCGAGGGCAGCTGGGAGATGTGTGTCACCTGGGGGAGGAGCGC	1876
Db	1904	TCAAGACCCAGGCCCATCAGGGCCACTGGAGAGAGGTGTGTGACTTTGGATGAGGAGCTC	1963
Qy	1877	CTTCCCACTCTACTACTGTCAGCTGGAGCCAGTGCCTGCTACTGCTTTCACCGAGCAGC	1936
Db	1964	TGAACACCCCTGCTACTGCACTAGAGGCTAAATCCTGCCACATCTCTGTGGACCAAGC	2023
Qy	1937	TGGGCGCTTTTGGCTGTGGGAGAGGCCCTCAGCGTGGCTGGCGGCAAGCGCTCAAGC	1996
Db	2024	TGGGTACCTACGTGTTTCAAGGGAGTCTTACTCTCCGCTCCGAGTCAAGCGCTCCAGC	2083
Qy	1997	TGCTTCTGTTTGGCGCGCTGCTGACCTCCCTCGAGTACAACTCCCGGCTCTACTGCC	2056
Db	2084	TAGCAATCTTGGCCCCAGCCCTCTGCACCTCTCTCGAGTATAGTCTCAGGGTCTTACTGC	2143
Qy	2057	TGCATGACACCCAGTATGCACTCAAGGAGGTGTGCACTGGAGAGCAGCTGGGGGAC	2116

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Db 2144 TGGAGGACACTCTCTGACGACCTGAAGGAGGTCTTAGAGCTGGAGAGACTCTGGGTGGCT 2203
Qy 2117 AGCTGATCCAGGAGCCACGGGTCTCTGCACTTCAAGGACAGTTACCAAACTCGGCTAT 2176
Db 2204 ACTTGGTGGAGGAGCCCAAGACTTGTCTCTTTAAGGACAGTTACCAAACTACG-CTCT 2262
Qy 2177 CCATCCACGATGTGCCAGCTCCCTGTGGAGAGTAGCTTCTGTGAGTACCAAGAGA 2236
Db 2263 CCCTCCATGACATCCCCCATGCCCCACTGGAGGAGCAAACTACTGGCCAAAGTACCAAGAGA 2322
Qy 2237 TCCCTTTTATCAATCTGGAATGGCACGCGAGGGTACTTTGCACTGACACCTTCAACCTGG 2296
Db 2323 TTCCCTTCTACCATGTGTGNAACGACAGCCAGAAAGCCCTGCACTGCACTTTCAACCTGG 2382
Qy 2297 AGCGTGTACGCCAGCACTAGTAGACCTGTGCTGCAAGCTGTGGGTGTGCAAGTGGAGG 2356
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Qy 2357 GCGAGGGGAGAGCTTACGATCACTCAATCTCAACATCAC--CAAGGACACAAGGTTTGCTG 2413
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Qy 2654 ACGGCAACCTCAGGACCTGGCTGACAGCTGGCTGAGCTGGGCGAGCCAGACGCTGGCC 2713
Db 2743 ATGGGGACCTCAACAGCTGGCCAGTGCCTTGGAGGAGATGGGCAAGAGTGAGATGCTGG 2802
Qy 2714 TCTTTCAGTGTGCGAGGCTGAGTGCTGA 2742
Db 2803 TAGCCATGACCACTGATGGCGATGCTGA 2831
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RESULT 7
US-09-949-016-4794
; Sequence 4794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4794
; LENGTH: 3008
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4794
Query Match 30.3%; Score 833.6; DB 4; Length 3008;
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Best Local Similarity 62.1%; Pred. No. 7.4e-177;
Matches 1435; Conservative 0; Mismatches 814; Indels 63; Gaps 5;
Qy 485 TGGCAGAGAACTTTCGAGCAGGAGCCGCTGGCCAAAGAGGTGTCTCTGGCAGCAGGCAATCG 544
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Qy 545 TGTGCTGCTGCTGCTCCACCGGAGGGCATTCCTCCAGCCGAGGTGGAGTGGCTCCGGAAACG 604
Db 70 TACTCCAGTGTGCAACCACTGAAGGATCCAGTGGCTGAGGTGGAATGTTGAAAAATG 129
Qy 605 AGACCTGTGTGAGCCCGTCCCTGGAACCCCAATCTATACATCACGCGGAGCAGACCTGG 664
Db 130 AAGACATAATTTGATCCCGTTGAAGATCGGAATTTTATATTACTATTTGATCACAACCTCA 189
Qy 665 TGTGCGGACAGGCCCGCTTGTCTGACACGCGCAACTACACCTGCTGGGCCAAGAAATCG 724
Db 190 TCATAAAGCAGGCCCGACTCTCTGATCTGCAATTTACACCTGTGTGCCAAAACATTG 249
Qy 725 TGGCAGTGTGCGCCGAGGCTCCGCTGTGCTGTGTCATTCGTCTAGTGAACGTTGGTGTGCGA 784
Db 250 TTGCCAAGAGGAAAGTACAACTGCCACTGTCTATAGTCTATGTCAACGGTGGCTGGTCCA 309
Qy 785 CGTGGACCGAGTGTGCTGCTGCGAGCGCCAGCTGTGGCGGCTGGCAGAAACGAGCC 844
Db 310 CTTGGAGCGGAGTGTGTGTGTAAACAGCCGCTGTGACGAGGGTATCAGAAACGTACAA 369
Qy 845 GAGCTGTGCACCAACCCGCGGCTCTCAACGGGGGCGCTTCTGTGAGGGGCGAGAATGTCC 904
Db 370 GGACTTGTACCAACCCGCGCACCCTCAATGGGGGTGCTTCTGTGAAGGCGCAGGTGTC 429
Qy 905 AGAAAACAGCTGCGGCCACCTGTGCCCAGTAGACGGGAGCTGGAGCCGTGGAGCAAGT 964
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Qy 965 GGTGCGCTGTGTGGCTGGACTGCACCCACTGGCGGAGCGTGTGAGTGTCTGTACCCAGCAC 1024
Db 490 GGTCTACTTGTGAACTGTAGTGACCACTGGCGCAGGAGGAGTGCACGGCGCCAGCCC 549
Qy 1025 CCGCAACCGAGGGGAGGAGTGCAGGGCACTGACCTGGAACACCCGCAACTGTACCAAGT 1084
Db 550 CCAAGAAATGGAGGCAAGGACTGCGACGGCTCTCTTGGCAATCCAAGAACTGCACATGATG 609
Qy 1085 ACCTCTGTGTACAGTGTCTTGGCGCTGGAGACGCTGGCCCTCTATGTGG---CCTCA 1141
Db 610 GGCTTTGCATGACAGTGTCTCTGATTCAGATGATGTGCTCTCTATTTGGGATTTGA 669
Qy 1142 TCGCCGTGGCGGTCTGCTGCTGCTGTCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCT 1201
Db 670 TAGCAGTGTGTTTGGCTGGCGATCTCTGTAGTGTGGCTTGTGTGTATCGGAGA 729
Qy 1202 AGAAGAGGGGCTGGACTCAGATGTGGCTGACTGCTGCATTTCTCACTCAGGCTTCAGC 1261
Db 730 ATCATCGTGACTTTGAGTCAGATATTATTGACTCTTTCGGCACTCAATGGGGGCTTTCAGC 789
Qy 1262 CCGTGAAGTCAAGCCCGCAAGCAGACACACCCCATCTGCTCAACCATCCAGCCGAGCC 1321
Db 790 CTGTGAACATCAAG-----GCAGCAAGACAAGATCTGTGGCTGTATCCCCCAGACC 840
Qy 1322 TCAGCAACCAACCAACCTACAGGCGAGTCTGTGTCCCCGGCAGGATG-----GGCC 1376
Db 841 TCAGCTCAGTGTGAGCCATGTACAGAGGACCTGTCTATGCCCTGCACTGAGCTCTCAGACA 900
Qy 1377 CAGCCCCAAGTTCAGACTCACCAAT----GGGCACCTGTCTCAGCCCTCGGTGGGCGGCC 1432
Db 901 AATATCCCAATGACCAACTCTCCAATTTCTGGATCCACTGCGCCAACTGAAAAATCAAAAGTGT 960
Qy 1433 GCCACACCTGACACAGCTCTCCCACTCTCAGGCGGAGGATTCGTTCTCCGCTCT 1492
Db 961 ACAACACCTCAGGTGTGTACCCCCCAAGATGACCTCTCTGAGTTTACCTCAAGCTGT 1020
Qy 1493 CCACCCAGAACTACTTTCGCTCCCTCCCGGAGGACCCAGCAACATGA-----1540
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Db 1021 CCCCTCAGATGACCCAGTGGTGTGGAGAAATGAAGCCCTCAGCTCGAAGAACAGAGTC 1080
Qy 1541 -----CCTATGGGACCTTCAACTTCCTCGGGGCC 1570
Db 1081 TAGCAGGACGACGTATCCATCCTGTACCGCAATTTGGCAGCTTCAACTTCGCTGGGAGTC 1140
Qy 1571 GGCTGATGATCCCTAATAAGTATCAGCTCCTCATCCCCCAGATGCCATACCCGAG 1630
Db 1141 ACCTTATTTGCCCAATTCAGGAGTCAGCTGTCTGATTTCCGCTGGGGCCATTCGCCAAG 1200
Qy 1631 GGAAGATCATAGATCTACCTCAGCTGACAGCGGAGAGAGTGAAGTTGCCCTAG 1690
Db 1201 GGAGAGTCTACGAAATGTATGTGATCTGTACACAGGAAAGAACTATGAGGCCACCCATGG 1260
Qy 1691 CTGGCTGTACAGCCCTGTGAGTCCCATCTGTAGCTGTGGACCCCTGGGCTCCTGTCA 1750
Db 1261 ATGACTCTCAGACACTTTTGACCCCTGTGTGAGCTGTGGGCCCCCAGAGCTCTGTCTCA 1320
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Db 1321 CCCGCCAGTGGTCTCTACTATGTATCACTGCGCAGACCCCCAATACCGAGGACTGGAAA 1380
Qy 1811 TGGCCCTCAAAAAGCAGTGTGCGAGGACGCTGGAGGATGTGTGACCTGTGACCTGGCGAGG 1870
Db 1381 TACTGCTCAAGAACCCAGCAGCAGAGGACAGTGGGAGGATGTGTGTGCTGGGGAGG 1440
Qy 1871 AGGCGCCTCCCACTCTACTACTGCCAGCTGGAGGCCAGTGCCTGTAGCTTTCACCG 1930
Db 1441 AAAACTTACACACCCCTGTCTACATTCAGCTGTGATGAGAGGCTGCCACATCTCAAG 1500
Qy 1931 AGCAGCTGGGCGCTTTGCCCTGTGGAGAGGCCCTCAGCGTGGCTCGCGCCCAAGGCC 1990
Db 1501 AGAACCTCAGCACCTACGCCCTGTGTAGGACATTCACCAACCAGAGCGCTGGAGCGCC 1560
Qy 1991 TCAAGCTGCTCTGTGTGGCGGCTGGCTGCACCTCCTCGAGTACAATCCGGGTCT 2050
Db 1561 TCAAGCTGGCCATCTTTGGGCCCCCTGTCTCTCTCGCTGGAGTACAGATCCGAGTCT 1620
Qy 2051 ACTGCCCTGCATGACACCCAGCATCAAGGAGGTGTGTCAGCTGAGAGAGCAGCTGG 2110
Db 1621 ACTGTCTGGATGACACCCAGGATGCCCTGAAAGAAATTTTACATCTTGAGAGACAGATGG 1680
Qy 2111 GGGACAGCTGATCCAGGAGCACGGGTCTGTCACTTCAAGGACAGTTTACCAACCTGC 2170
Db 1681 GAGGACAGCTCCTAGAAAGACCTAAGGCTCTTCAATTTAAGGACAGCACCAACCTGC 1740
Qy 2171 GCCTATCCATCCAGATGTGCCAGCTCCCTGTGGAAAGATGAAGCTCCTGTGAGTACC 2230
Db 1741 GCCTGTCAATTCAGATATCGCCCATTCCTCTGGAAGAGCAATTTGCTGCTAAATATC 1800
Qy 2231 AGGAGATCCCTTTTATCAGATCTGGAATGGCAGCGAGCGGTACTTGCAGTGCACCTTCA 2290
Db 1801 AGGAATTTCAATTTTACATGTTTGGAGTGGATCTCAAGAAACCTGACCTGCACCTTCA 1860
Qy 2291 CCCTGGAGCGTGTGAGCCCCAGCAGTGTAGTACCTTGGCTTGAAGCTGTGGGTGGCAGG 2350
Db 1861 CTCTGGAAAGATTTAGCTTGAACACAGTGGAGCTGTTTGAACACTCTGTGTGGCGAGG 1920
Qy 2351 TGGAGGGCGAGCGGACAGCTTACAGCATCAACTTCAACATCAACAGGACACAGGTTTG 2410
Db 1921 TGGAAAGGAGAGGGCAGATCTTCCAGCTCAACTGCACCTGTTCAGAGGAACTTACTGGCA 1980
Qy 2411 CTGAGCTGTGGCTCTGAGAGTGAAGCGGGGTCCAGGCCCTGTGGTGGGCCCCAGTGCCT 2470
Db 1981 TCGATTTGCGCTGCTGATCTCCGAAACCATCACAGGTCACGGGGCCAGTGCCT 2040
Qy 2471 TCAAGATCCCTTCTCATTTGGCAGAGATTAATTTCCAGCTTGGACCCACCTGTAGGC 2530
Db 2041 TCAGCATCCCTCTCCCTATCCGGCAGAGCTCTGTAGCAGCTGTAAGTCCCCAGCAGA 2100
Qy 2531 GGGGTGCGGACTGGCGGACTCTGCGCCAGAAATCTCCACCTGGAAGCAGCATCTAGCTTCT 2590
Db 2101 GAGGCCATGACTGGAGGATGTGCGCCATAAGCTGAACTGGAAGCTTGAATTAAT 2160

Qy 2591 TTGCTCTCAAGCCAGCCCCACAGCCATGATCTCTCAACTGTGTGGAGCGCGGCACTTCC 2650
Db 2161 TTGCCACAAATCAGGCCCACTGGCGTATCTCTGGATCTTTTGGGAAGCAGAACTTCC 2220
Qy 2651 CCAACGGCAACCTCAGCAGCTGGCTGACAGCAGTGGCTGGACTGGGCCAGCAGACGCTG 2710
Db 2221 CAGATGGAACCTCTGAGCATGCTGGCAGCTGTCTTTGGAAGAAATGGGAAGACATGAACGG 2280
Qy 2711 GCCTCTTCAAGTGTGGAGGCTGAGTGTCTGA 2742
Db 2281 TGGTGTCTCTAGCAGCAGAGGGCGAGTATTAA 2312

RESULT 8

US-09-969-532-9

; Sequence 9, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 2736

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-969-532-9

Query Match 17.7%; Score 487; DB 4; Length 2736;

Best Local Similarity 50.9%; Pred. No. 2.7e-99;

Matches 1305; Conservative 0; Mismatches 1230; Indels 30; Gaps 5;

Qy 172 CTTCCCCACTTCTGTGGAGCCCGAGGATGTGTACATCTCAAGAACAGCCAGTCTG 231
Db 157 CTGCCTCATTTATAGAGGAGCAGATGATGTATATTATCAAGAGCAACCTTATTGCA 216
Qy 232 CTGTGTGCAAGCCGTCGCCGCCACGACATCTTCTTCAAGTGCACGAGAGTGGTG 291
Db 217 CTGAGTGTCAAGCGAGCCAGCCATGACATATTTCTTCAATGCAACGCGAGTGGTC 276
Qy 292 CGCCAGTGGACCACTGTATCGAGCGCAGCAGCGGAGCAGTGGGCTGCCACCATG 351
Db 277 CATCAGAACGAGCAGCTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCGC 336
Qy 352 GAGTTCGGATTAATGTCTCAAGGCGAGGTCGAGAGGTGTTCGGGCTGGAGGAATAC 411
Db 337 GAAGTGTTCATCAATGTACTAGGCAACAGGTGGAGACTTTCATGGGCCCGAGGACTAT 396
Qy 412 TGTGTCAGTGTGGCATGAGCTCTCTCGGGCACCAAGAGTCAAGAGGCTTACATC 471
Db 397 TGTGCCAGTGTGGGTGGAGCCACCTGGGTACCTTCAAGAGCAGAGGCTCTGTG 456
Qy 472 CGCATAGCCAGATTGCGCAAGAACTTTGAAACAAGACCCACAAGAGGAGGTGTCCCTG 531
Db 457 CGCATAGCTTATTTACGGAACAACTTTGAAACAAGACCCACAAGAGGAGGTGTCCCAT 516
Qy 532 GAGCAGGACATCTGTCTGCCCTGCCCTCCAGCCGAGGACATCCCTCCAGCCGAGGTGAG 591
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Qy 592 TGTCTCGGAACGAGGACCTGTGGACCCGCTCTGACCCCAATGTATACATCACCGCG 651
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Qy 652 GAGCAGAGCTGTGTGGTGGACAGGCGCCCTTGTGTGACACGCGCAACTACCTGCTGTG 711

Db 637 GACCATAACTGATCATCAGCAGGACGGCTCTCGACTCAGGAATTAACACTGATG 696
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712 GCCAAGAACATCGTGGCACTGCGCGCAGCGCCTCGCTGCTGTCACTGCTGTAAC 771
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697 GCAGCCAACTCGTGGCTAAGAGGAGAAGCTGTGCGCCACTGTGTGGTCTACGTGGAT 756
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772 GGTGGGTGGTGGAGTGGACCGAGTGTGCTGTGAGCCGACAGTGTGTGGCGGGGTGG 831
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757 GGGAGCTGGGAAGTGTGGAGCGAATGGTCTGCTGCAAGTCCAGAGTGTGA-----A 807
Qy
832 CAGAAACGAGAGCGAGCTGCACCAACCGCGCTCTCAACGGGGCGCTTTCTGTGAG 891
Db
808 CATTTGGGATCCGGAGTGCACGACACACCCCGGAGAAATGGGGCAAAATCTGTGAA 867
Qy
892 GGGCAGAAATCTCCAGAAAAACAGCTGTGCGCCACCTGTGCCCCAGTAGACGCGAGTGGAGC 951
Db
868 GGTCTAAGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGGCATCTCCAGATAAAAAACCT 927
Qy
952 CCGTGGAGCAAGTGGTGGCGCTGTGGCTGGACTGTGACCTGACCCACTGGCGGAGCCGTGAGTC 1011
Db
928 CTTTCATGAAATAAAACCCCAAGCATTTGGAATGCGCAGGACATTTGCTTTGTAATCGGGC 987
Qy
1012 TCTGACCCAGCACCCCGCAACGAGGGAGGAGTGGCAGGGCACTGCACCTGGACACCCGC 1071
Db
988 TTGGGTCTGCGCTGTGGCGTTGCAATCTTGGTCAATTTGGTGTCACTTACAGAGG 1047
Qy
1072 AACTGTACCAAGTACCTCTGTGTACACAGTGTCTTGGCCCTGTGAGAGAGTGGCCCTCTAT 1131
Db
1048 AGCCAGAGTGAATGTCGTGGAGCTCATTTCACTCTTCTGCAATGACAGGTGGCTTCCA- 1106
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1132 GTGGGCTCATCGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
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1107 --GACCTTCAACTTCAAAACAGTCCGTCAGGCCAAGAAATATCATGGAACAAATGATACAA 1164
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1192 TATTTCCGGAAGAAGGAGGGCTGGACTCAGATGTGGCTGACTCGTCTCAATTTCTCACCTCA 1251
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1165 GAAAAATCCTTTGGTAATCCCTGCTCTGAAATCTGCCATGCGCCAGATCTGCANGTG 1224
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1252 GGCTTCAGCCCGTACAGATCAAGCCCAAGCAAGAGAGCAACCCCAATCTGTCAACATC 1311
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1225 AGCCGACATACAGCGGACCCATCTGTCTGAGGACCTCTGAGCAAGAGGCTCATGACA 1284
Qy
1312 CAGCCGACCTCAGCACCAACCACTTACAGGGCAGTCTGTCTCCCGGAGGAT 1371
Db
1285 GAGTCTCTACTTTTAACTTTTGTGCGGACATCAAGTGAAGTCCAGAGCTCTGTCATG 1344
Qy
1372 GGGCCCAAGCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCTCGGGTGGCGGC 1431
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1345 GTTTCCCTGGGAGTGTCTGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1404
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1432 CGCCACACCTGCACACAGCTCTCCCACTCTGAGGCGGAGAGTTCGTCTCCCGCTC 1491
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1405 CCCCATGAAACACCAACAGCTTTAGTACATGATGATGATGATGATGATGATGATGATGATGAT 1464
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1492 TCACCCAGAACTACTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1551
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1516 TTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCA 1575
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1612 CCAGATGCCATACCCGAGGAGAGTCTATGAGATCTACCTCAGCTGCAAGAGCCGGA 1671
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1576 CACGGTGCCTCCAGAGGAGAAATTTCTGGGAGATTTATATGTCCAT---CAACCAAGGT 1632
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1672 GACGTGAGGTGTGCCCTAGCTGGCTGTGACACCTGCTGAGTCCCATCTGTAGTGTGGA 1731
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1633 GAACCCAGCTCCAGTCAGATGAGCTGTGAGTGTCTGAGTCTCTGAGTCACTGTGAGT 1692
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1732 CCCCCTGGCTCTGCTCACC CGGCCAGTCACTCTGCTATGGAACCACTGTGGGAGGCC 1791
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Qy 1792 AGCCCTGACAGCTGGAGCTGCGCTCAAAAAGAGAGTGTGTGAGGGCACTGGAGGAT 1851
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1753 AGTTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACAGCAGGGCAAAATGGAGAA 1812
Qy
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1813 GTGATGTCAAGTGAAGATGAATCTATCATC-----CTGTACTGCTTTTGGACCCCTTT 1866
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1912 GCCTGTCTAGCTCTTCCAGCAGAGCTGGGCGCTTTTGGCTGTGGAGAGGCGCTCAGC 1971
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1867 GCGTGTCTGTCTCTGACAGCTTTGGACCTATGCGCTCACTGGAGAGCCAAATCACA 1926
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1972 GTGGCTGCGGCCAAAGCGCTCAAGCTGTCTTGTGTGGCGCGGTGCTGCACTCCCTC 2031
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1927 GACTGTGCGCTGGAAGCAATGAAGTGGCGGTTTTGGCTGCTGCTGTAATCTCCCTG 1986
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2032 GAGTACAACTCCGGGTCTACTGCTGATGACACCCAGATGCACTCAAGGAGGTGGTG 2091
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2167 AAACCAATCTACTGCTGCGAGAGTCCCGTCTCCGCGTGTGTGAGTAAACCGCAG 2226
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2512 CTGGACCCACCTGTAGGGGGTGGGAGTGGGAGTCTGGCCCGAGAACTCCACCTG 2571
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2692 CTGGCCAGCCAGAGCTGGCTCTTCAAGTGTGCGAGGCTGAG 2736
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2647 ATTTGGAGGAGACACACGAAACTCTCAAAATTTCAAAATTTCCAGATCCCAG 2691

RESULT 9

US-09-969-532-33
; Sequence 33, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 677723261 Human Membrane Proteins and Polynucleotides Encodinf

; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-969-532-33

Query Match 17.7%; Score 487; DB 4; Length 3411;
Best Local Similarity 50.9%; Pred. No. 2.9e-99;
Matches 1305; Conservative 0; Mismatches 1230; Indels 30; Gaps 5;

Qy	172	CTTCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAGCCAGTGTCTG	231
Db	271	CTGCCTCATTTTCAATAGAGGAGCCAGATGCTTATATATCAAGAGCAACCTTATTGCA	330
Qy	232	CTTGTGTGCAAGCCGTCGCCGCCACGAGATCTTCTCAAGTCAAGGGGAGTGGTG	291
Db	331	CTCAGGTGCAAGCGAGGCCAGCCATGAGATATTTCTTCAATGCAACGGCGAGTGGGTC	390
Qy	292	CGCCAGGTGGACACAGCTGATCGAGCGGACGACACAGCGGAGCAGTGGGCTGCCACCATG	351
Db	391	CATCAGAACGACAGCTCTGAAAGACTCTGACGAGAGCTCAGGTTTGAAGGTCGCG	450
Qy	352	GAGTCCGCAATTAATGTCTCAAGGACGAGGTGAGAGAGGTTCGGGGCTGGAGGAATAC	411
Db	451	GAAGTGTTCATCAATGTTACTAGSCAACAGCTGGAGGACTTCATGGGCCCGAGGACTAT	510
Qy	412	TGTTGCCAGTGTGGATGAGTCTCTCGGGACCAACCAAGAGTCAAGAGGCTCATC	471
Db	511	TGGTGCCAGTGTGGGGTGGAGCACCTGGGTACTCTCAAGAGCAGAGGCGCTCTGTG	570
Qy	472	CGCATGCCAGATTGGCAGAACTTCAGCAGAGCGGCTGGCCAAAGGAGGTGTCCTG	531
Db	571	CGCATAGCCTATTACGGAATACTTTGAACAAGCCCAAGAGAGGGAAGTTCCTCAT	630
Qy	532	GAGCAGGACATGCTGTGCTGCTGCGTCCACCGAGGGGATCCCTCCAGCGCGAGGTGGAG	591
Db	631	GAAGGCATGATTGTACTGCACTGCGGCCACCGAGGGAGTCCCTGTGTCGAGGTGGAA	690
Qy	592	TGCTCCGGAACGAGGACCTGTGGACCGTCTCGGACCCCAATGTATACATCAGCGGG	651
Db	691	TGGCTGAAAATGAAGAGCCCATTTGACTCTGAAACAAGACGAGAACATTTGACACCGGGCT	750
Qy	652	GAGCAGACCTGTGTGGTGGACAGGCGCGCTTGTGACACGCGCAACTACCTGCGTG	711
Db	751	GACCATTAACCTGATCATCAGCAGGACCGGCTCTGGAGCTCAGGAATTAACCTGCA	810
Qy	712	GCCAAGAACATCTGTGGCAGCTGCGCGCAGCGGCTCCGCTGCTGTCTATCTGCTACGTTAAC	771
Db	811	GCAGCCAACTCTGTGCTAAGAGGAGAAGCTGTGGCCACTGTGTGGTCTACGTGGAT	870
Qy	772	GGTGGTGTGTCAGTGGACCGAGTGTGCTGTGACAGCCGACAGTGTGGGCGGCTGG	831
Db	871	GGGAGCTGGGAAGTGTGGAGCAATGTGCTGTGCAAGTCCAGAGTGTGA-----A	921
Qy	832	CAGAAACGAGCGGAGCTGCACCAACCGCGGCTCTCAACGGGGGCTTTCTGTGAG	891
Db	922	CATTTCGGATCCGGAGTGCACAGCACACCCCGAGAAATGGGGGCAAAATTTCTGTGAA	981
Qy	892	GGGCAGAAATCTCCAGAAAAACAGCCCTGCGCCACCTGTGCGCCAGTAGACGCGAGCTGGAGC	951
Db	982	GETCTAAGCCAGGAATCTGAAACTGCAACAGATGGTCTTTGCACTCTTAGATAAAAACCT	1041
Qy	952	CCGTGGAGCAAGTGTGGGCTGTGGGCTGGAGTGCACCACTGGCGGAGCGGTGATGC	1011
Db	1042	CTTCAATGAAATAAAACCCCAAGCATTTGAGAAATGCCAGCGACATTTGTTGTACTCGGGC	1101

Qy	1012	TCTGACCCAGACCCCGCAACGGAGGGAGGAGTGCACGGGCACTGACCTGGACACCGCG	1071
Db	1102	TTGGGTGCTGCGCGTCTGGGCGTTTGCAGTCTCTGGTCAATGGTGTACACCTTTACAGCGG	1161
Qy	1072	AACGTGTACCACTGACCTCTGTGTACACAGTGTCTTCTGGCCCTGAGGAGCTGGCCCTCTAT	1131
Db	1162	AGCCAGAGTGAATGATGCGGTGGAGCTATTGACTCTTCTGCAATTGACAGGTGGCTTCCA-	1220
Qy	1132	GTGGGCTCATCGCGGTGGCGGTCTGCTGTCTGCTGTCTGCTGTCTGCTCATCTCTGTT	1191
Db	1221	--GACCTTTCAACTTCAAAACAGTCCGTCAAGCCCAAGAAATATCATGGAACCTAATGATACAA	1278
Qy	1192	TATTTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGTGTGCTGCTCATTTCTCACCTCA	1251
Db	1279	GAATAATCTTTGTGTAATACTCCCTGCTCTGAAATCTTCCCATGAGCCAGATCTGACAGTG	1338
Qy	1252	GGCTTCCAGCCCGTCAAGCTCAAGCCCAAGCAAGCAGACCAACCCCACTCTGCTCACCATC	1311
Db	1339	AGCGGACATACAGCGGACCCATCTGTCTGAGGACCTCTGGACAGGAGCTCATGACA	1398
Qy	1312	CAGCGGACCTCAGCACCACCAACCACTACAGGGGAGTCTCTGTCTCCCGGAGGAT	1371
Db	1399	GAGTCTCTCACTCTTTAAACCTTTTTCGGACATCAAAGTGAAGTCCAGAGCTCTGTCATG	1458
Qy	1372	GGGCCAGCCCAAGTTTCCAGCTCACCAATGGGACCTGCTCAGCCCTGGTGGCGGC	1431
Db	1459	GTTCCTTGGGAGTGTCTGAGAGAGTGAATCACCGGCAAGAAATCATTCAGGACTTTT	1518
Qy	1432	CGCCACACACTGCACACACAGCTCTCCCACTCTGAGGCGGAGGAGTTCTGCTCCCGCTC	1491
Db	1519	CCCATGGAACAAACACAGCTTTAGTACAATGCATCCCAAGAAATAAATGCCCTACATC	1578
Qy	1492	TCACCCAGAACTACTTTCCTGCTCCCTGCCCCGAGGACACAGCAACATGACTATGGGACC	1551
Db	1579	CAAAATCTGTC-----ATCACTCCCAAGGACAGAACTGAGGAGCAACTGTGTGTC	1629
Qy	1552	TTCAACTTCTCGGGGCGGCTGATGATCCCTTAATACAGGTATCAGCCCTCTCATCCCC	1611
Db	1630	TTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCA	1699
Qy	1612	CCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAGCCCGGAA	1671
Db	1690	CACGGTGCCATCCAGAGGAGATTTCTGGAGATTATATGTCCAT--CAACCAAGGT	1746
Qy	1672	GAGTGAGGTGGCCCTAGCTGTGTGACAGCCCTGTGTAGTCCCATCTGTTAGTGTGGA	1731
Db	1747	GAACCCAGCCTCCAGTCAAGTGGCTCTGAGGTGCTCTGAGTCTCTGAAGTCACTGTGTT	1806
Qy	1732	CCCCCTGGGTCTCTGCTCAGCCCGCAGTCTATCTTGGCTATGACCACTGTGGGGAGCCC	1791
Db	1807	CTTCCAGACATGATCTGACCACTCTCTTGTGATTTGACCATCCCGCATCTGCAATGTCT	1866
Qy	1792	AGCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCTGTGCGAGGCGAGCTGGAGGAT	1851
Db	1867	AGTTCTGAGCATTTGGAAATATCCATTTAAGAAAGGACACAGCAGGGCAATGGAGGAA	1926
Qy	1852	GTGCTGCACTTGGGCGAGGAGCGCCCTCCCACTCTACTCTGCAAGTGTGGAGGCGAGT	1911
Db	1927	GTGATGTGAGTGAAGATGAATCTATCATC-----CTGTACTGCTCTTTTGGACCCCTTT	1980
Qy	1912	GCCTGTAGTCTTCAACCGAGCAGTGGGCGCTTTGGCTGTGGGAGGAGGCGCTCAGC	1971
Db	1981	GCCTGTAGTGTCTCTGACAGCTTTGGAGACCTATGCGCTCACTGGAGAGCAATCACA	2040
Qy	1972	GTGGCTGCGCCCAAGCGCCTCAAGCTGCTTTCTGTTTGGCGCGGTGCGCTCAGCTCCCTC	2031
Db	2041	GACTGTGCGGTGAAGCACTGAAGTGGCGGTTTGGTGGCTGCTGCTGTAATCTCCTG	2100
Qy	2032	GAGTACAACTCCGGTCTACTGCTGCTGATGACACCAAGTCACTCAAGAGGAGGTGGT	2091
Db	2101	GATTACAACTGAGATTTACTGTGTGGACAAATACCCCTTGTGCTATTTTTCAGGAAGTGGT	2160

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QY 2092 CAGCTGGAGAACGAGCTGGGGGAGCAGCTGATCCAGAGAGCCACGGGTCTCTGCACTTCAAG 2151
Db 2161 TCAGATGAAGAGGATCAAGGTGACACAGCTCCTGGAAGAACCAAAATTGCTGCAATTTCAAA 2220
QY 2152 GACAGTTTACCACAACTTGGCCCTATCCATCCAGATGTGCCAGCTCCCTGTGTGGAAGAGT 2211
Db 2221 GGGNATACCTTTAGTCTTCAGATTTCTGTCTTGATATTCCCCATTCCTCTGGAGATT 2280
QY 2212 AAGCTCCTTGTCACTACCAAGAGATCCCTTTTATACATCTGGAATGCCACGACGG 2271
Db 2281 AAACCAATTCATGCTGCTGCCAGGAAGTCCCGTTCTCCCGCTGTGGTGCAATAACCGCAG 2340
QY 2272 TACTTGACATGCACCTTCACCTCGAGCGTGTAGCCCGCAGCACTAGTGACCTGGCTGC 2331
Db 2341 CCCTGACATGTGCTTCTCCCTGAGCGTTATACGCCCACTACCAACCCAGCTGTCTGTC 2400
QY 2332 AAGCTGTGGTGTGGCAGGTGGAGGCGACGGGCGAGAGCTTCAGCATCAACTTCAACATC 2391
Db 2401 AAAATCTGCATTCGGCAGCTCAAGGCCATGAAGCCATGACAGATCTCCAGTGCAGATCAATC 2460
QY 2392 ACCAAGGACACAAGGTTTGTGAGTGTCTGGTCTGGAGAGTGAAGCGGGGTCCCAAGCC 2451
Db 2461 CTAGAGAGTCAAGCAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTCCCTGCA 2520
QY 2452 CTGGTGGGCCCCAGTGCCTTCAGATCCCTTCTCATTCATTCGGCAGAGATAATTTCAGC 2511
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QY 2512 CTGACCCACCTGTAGCGGGGTGCGCACTGGCGGACTCTGGCCCCAGAACTCCACCTG 2571
Db 2581 TTTGATACCCCAATGCCAAGGCAGGACTTGGCAGATGTAGCAGAAAGACAGCATC 2640
QY 2572 GACAGCCATCTAGCTTCTTTGCTCCAAAGCCAGCCCCACAGCATGATCTCAACCTG 2631
Db 2641 AACAGGAATTTATCTTATTTTCGTACACAAAGTAGCCCATCTGTCTCATTTTGAACCTG 2700
QY 2632 TGGGAGCGGGCACTTCCCAAGCCAACTCAGCAGCTGCTGCGCAGTGGCTGGA 2691
Db 2701 TGGAGCTCGTCATCAGATGATGTGATCTTGACTCCCTGGCTGTGCTTGAAGAG 2760
QY 2692 CTGGCCAGCAGACGCTGGCTCTTCCACAGTGTGGAGGCTGAG 2736
Db 2761 ATTGGGAGGACACACAGAACTCTCAACATTTCAAGATCCCGAG 2805

RESULT 10
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-11

Query Match 17.0%; Score 467; DB 4; Length 2703;
Best Local Similarity 51.0%; Pred. No. 8.1e-95;
Matches 1307; Conservative 0; Mismatches 1195; Indels 63; Gaps 6;

QY 172 CTTCCCCACTTCTGGTGGAGCCGAGGATGTGTACATCGTCAGAAACAAGCCAGTGTCTG 231
Db 157 CTGCTCATTTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCCTATTGCA 216
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QY 232 CTTGTGTGAAGCCCGTGTGCCCGCCACGCAAGATCTTCTTCAAGTGCACACGGGAGTGGGTG 291
Db 217 CTGAGGTGCAAGCGAGGGCCAGCCATGCAGATATTTCTTCAATGCAACCGCGAGTGGGTG 276
QY 292 CGCAGGTGGACCACTGTATCGAGCGCAGACAGCGGAGCAGTGGCTGCCACCATG 351
Db 277 CATCAGAACGAGCAGCTCTCTGAAGAGACTCTCGACGAGAGCTCAGGTTTGAAGGTCCGC 336
QY 352 GAGGTCGCGATTAATGTCTCAAGGCGACAGGTTCAGAAAGGTGTTCGGGCTGGAGGAATAC 411
Db 337 GAGTGTTCATCAATGTACTAGGCAACAGGTGAGGACTTCCATGGGCCCGAGGACTAT 396
QY 412 TGTGTCAGTGTGCGATGAGAGTCTCTGGGCAACACCAAGAGTCAAGAGGCTTACATC 471
Db 397 TGTGTCAGTGTGTGGGTGGAGCCACTGGGTACCTTCCAAAGAGCAGGAGGCTCTGTG 456
QY 472 CGCATAGCCAGATTTCGCAAGAACTTCGAGCAGAGCGCTGCCCAAGGAGGTGCCCTG 531
Db 457 CGCATAGCCATTATTACGGAATACTTTGAACAAGACCCCAAGAAAGGAGGTTCCTATT 516
QY 532 GAGCAGGGCATCTGTCTGCCCTCCAGCCGAGGGCATCCCTCCAGCCGAGGTGGAG 591
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QY 592 TGGCTCCGGAAACGAGGACCTGTGTGAGCCGCTCCCTGGACCCCAATGTATATACATCACCGG 651
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Db 1312 GTTTCCTCGGAGTGTCTGAGAGAGCTGAGTACACACGGCAAGAAATCATTCAGAGACTTTT 1371
Qy 1432 CGCCACACATGACACACAGCTCTCCACCTCTCAGAGCCGAGGAGTTGCTCTCCGCGTC 1491
Db 1372 CCCATGGAACAACACACAGCTTTAGTACAATGATCCAGAAATAAATGCCCTACATC 1431
Qy 1492 TCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCCACAGCAACATGACCTATGGGACC 1551
Db 1432 CAAAATCTGTC-----ATCACTCCCCAAGGACAGAACTGAGSACAACCTGGTGTG 1482
Qy 1552 TTCAACTCTCGGGGGCGGCTGATGATCCCTAATACAGTATACAGCTCTCCTCATCCCC 1611
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Qy 1732 CCCCCTGGCTCTGCTCAACCCGCCAGTCACTCTGGCTATGAGACCACTGTGGGGAGCCC 1791
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Db 1834 CGCTGTATGTGCTCTCGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGGCCAATCACA 1893
Qy 1972 GTGCTCCCGCCAGCGCTCAAGCTGCTTCTGTTTGGCGGTCGCTGCACCTCCCTC 2031
Db 1894 GACTGTCCGTGAAGCAACTGAAGTGGCGTTTTTGGCTGCACTGTCTGTAATCCCTGT 1953
Qy 2032 GAGTACAAACATCCGGGTCTACTGCTGCAATGACACCCACCGATGCACTCAAGGGAGTGGTG 2091
Db 1954 GATTACAACTTGAGAGTTTACTGTGTGCAAAATACCCCTTTGTGCAATTCAGGAAGTGT 2013
Qy 2092 CAGCTGAGAAAGCAGCTGGGGGACAGCTGATCAGAGAGCAGCGGTCTGCACTTCAAG 2151
Db 2014 TCAGATGAAGAGCATCAAGGTGGAAGCTCTCGTGAAGAACCATAATTTGCTGCAATTTCAA 2073
Qy 2152 GACAGTTTACCACACCTCGCGCTATCAATCACCAGATGTCACCTCCCTGTGGAAAGT 2211
Db 2074 GGGAAATACCTTATGCTTTCAGATTTCTGCTTGATATTTCCCCCATTTCTCTGGAGATT 2133
Qy 2212 AAGCTCTGTGCTACCAAGGAGATCCCTTTTATACATCTGGAATGGCAGCGAGCGG 2271
Db 2134 AAACCAATTCAGCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGTGTCAGTAAACCGGACG 2193
Qy 2272 TACTTGACATGCACTTTCAACCTGGAGGTGTGAGCCCCAGCACTAGTGAACCTGGCCCTGC 2331
Db 2194 CCCCCTGCACTGTGCTTTCTCCCTGGAGGTTTATACGCCCACTACCAACCCAGCTGTCTGTC 2253
Qy 2332 AAGCTGTGGGTGTGCGCAGGTGGAGGCGAGCGGCGAGAGCTTTCAGCATCACTTCAATC 2391
Db 2254 AAAATCTGCATTCGGCAGCTCAAAAGGCCATGAACAGATCTCTCCAAAGTGCAGACATCAATC 2313
Qy 2392 ACCAAGGACACAAGGTTTGTGCTGTGCTCTGGAGAGTGAAGCGGGGTCCAGCC 2451
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Db 2314 CTAGAGAGTGAACGAGAAACCATCACATTTCTTGSCAACAGGAGACAGCACATTTCCCTGCA 2373
Qy 2452 CTGGTGGGCCCCAGTGGCTTCAAGATCCCTTCTCTATTTCGGCAGAAAGATTAATTTCCAGC 2511
Db 2374 CAGACTGGCCCCCAAGCCTTCAAAATTTCCCTACTCCATCAGACAGCGGATTTGTGCTACA 2433
Qy 2512 CTGACCCACCTGTAGCGGGGTGCGACTTGGCGGACTCTGGCCAGAAACTCCACCTG 2571
Db 2434 TTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCAGAGAAAAACAGCATC 2493
Qy 2572 GACAGCCATCTCAGCTTTCTTGGCTTCAAGCCAGCCCCACAGCATGATCTCTCAACCTG 2631
Db 2494 AACAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCTGCTGTCAATTTTGAACCTG 2553
Qy 2632 TGGGAGCGGCGGCACTTCCCAACGGCAACCTCAGCAGCTGGCTGCAGCAGTGGCTGGA 2691
Db 2554 TGGGAAGCTCGTCAATCAGCATGATGATGATCTTGACTCCCTGGCCTGTGCCCTTTGAAGAG 2613
Qy 2692 CTGGGCCAGCAGACGCTGGCCTCTTTCAGAGTGTGGAGGCTGAG 2736
Db 2614 ATTGGGAGGACACACAGGAACCTCTCAAAATTTTCAGATCCCGAG 2658
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RESULT 11

US-09-969-532-13

; Sequence 13, Application US/09969532

; Patent No. 677232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13

; LENGTH: 2694

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-969-532-13

Query Match 16.7%; Score 460.2; DB 4; Length 2694;

Best local Similarity 51.94; Pred. No. 2.7e-93;

Matches 1330; Conservative 0; Mismatches 1163; Indels 72; Gaps 10;

Qy	172	CTTCCCCACATTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAAACAAGCCAGTGTCTG	231
Db	157	CTGCTCATTTTCATAGAGGAGCCAGATGCTTATATTATCAAGAGCAACCTATTGCA	216
Qy	232	CTTGTGTGAAGCCGCTGCCCCCAGCAGATCTTCTTCAAGTGCACGCGGAGTGGGTG	291
Db	217	CTCAGGTGCAAGCGAGGCCAGCCATGTCAGATATTTCTCAAATGCAACGCGCAGTGGTCT	276
Qy	292	CGCCAGGTGACACCACTGATTCGAGCCGACACAGACGGGAGCAGTGGCTGCCACCATG	351
Db	277	CATCAGAACGAGCACGCTCTCTGAAGAGACTCTCGACGAGAGCTCAGGTTTGAAGGTCCGC	336
Qy	352	GAGTTCGCAATTAATGTCTCAAGCGACAGGTGCGAAGGTGTTTCGGGCTGGAGGAATAC	411
Db	337	GAAGTGTTCATCATGTTACTAGGCAACAGTGGAGGACTTCATATGGCCCCGAGGACTAT	396
Qy	412	TGTTGCCAGTGTGTCGATGGAGCTCTCTCGGGCACCAACAGAGTCAAGAGGCTCATC	471
Db	397	TGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAAGCAGAGGAGGCTCTGTG	456
Qy	472	CGCATAGCCAGATTGCGCAAGAACTTCGACGACAGGCCGCTGGCCAGGAGGAGTGTCTCCTG	531
Db	457	CGCATAGCTTATTACGGAAAACTTTTGAACAAGACCCACAGAGGAGGAGTGTCCCATTT	516

Db 2605 ATTGGGAGGACACACGAAACTCTCAACATTTTCAGAAATCCCG 2649

RESULT 12

US-09-969-532-15

; Sequence 15, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 2661

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-969-532-15

Query Match 16.0%; Score 439.8; DB 4; Length 2661;

Best Local Similarity 51.2%; Pred. No. 9.9e-89;

Matches 1313; Conservative 0; Mismatches 1147; Indels 105; Gaps 8;

Qy 172 CTTCCCCACTCTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAGCCAGTCTG 231

Db 157 CTGCCTCATTTTCATAGAGGAGCCAGATGTCTTATATATCAAGAGCAACCCCTATTGCA 216

Qy 232 CTTGTGTGCAAGGCGGTGCCGCCACGACATCTTCTCAAGTGCACAGGGAGTGGGTG 291

Db 217 CTAGGTGCAAGGAGGCGCCAGCCATCGAGATATCTTCAATGCAACGGGAGTGGTC 276

Qy 292 CGCCAGGTGGACCAAGTGTGAGCGGACGACAGACGAGGAGTGGGCTGCCACCATG 351

Db 277 CATCAGAAACGAGCAGCTCTCTGAAGAGACTCTGACGAGAGCTCAGGTTTGAAGTCCGC 336

Qy 352 GAGTCCGCATTATGTCTCAAGCAGCAGGTGAGAGGTGTTCGGGCTGGAGGAATAC 411

Db 337 GAAGTGTTCATCAATGTCTTAGGCAACAGGTGGAGACTTCCATGGGCCCGAGGACTAT 396

Qy 412 TGGTCCAGTGTGGCATGAGTCTCTCGGGACACCAAGAGTCAAGAGGCGCTACATC 471

Db 397 TGGTCCAGTGTGGCGTGGAGCCACTGGTACCTCCAGAGCAGAGAGGCTCTGTG 456

Qy 472 CGCATAGCCAGATTGCGCAAGAACTTCAGCAGAGAGCGCTGGCCAGAGGAGTGTCCCTG 531

Db 457 CGCATAGCTATTATTACGGNAAAACCTTTGAAACAAGACCCACAAGGAGGGAAGTTCCCAT 516

Qy 532 GAGCAGGCGATGCTGCTGCCCTGCGCTCCACCGAGGGCATCCCTCCAGCGAGGTGGAG 591

Db 517 GAAGGCGATGATTGACTGCACTGCGGCCCAACAGAGGGAGTCCCTGCTGCCGAGGTGAA 576

Qy 592 TGGCTCCGGAACGAGGACCTGTGTGACCCGCTCGGACCCCAATGTATACATCACCGCG 651

Db 577 TGGCTGAAAATGAGAGCCATTGACTCTGAAACAAGCAGAAATGTGACACAGGGCT 636

Qy 652 GAGCAGCTGTGGTGTGCGCAGGCGCGCTTGTCTGACACGCGCAACTACCTGCGGTG 711

Db 637 GACCATAACCTGATCATCAGGAGGCGGCTCTCGGACTCAGGAAATTAACCTGCATG 696

Qy 712 GCCAAGAACATCTGGGACAGCTGCGCGGAGCGCTCCGCTGTGTCTATCGTGAAC 771

Db 697 GCAGCCAACTCTGTGGTGAAGAGAGAGCGCTGTGCGGCCACTGTGTGGTCTACGTGGAT 756

Qy 772 GGTGGGTGTGACGTGAGCCAGTGTCTCGTCTGACAGGCGCAGCTGTGGGCGGCGTGG 831

Db 757 GGGAGCTGGGAGTGTGAGGGAATGGTTCGTCTGCAAGTCCAGAGTGTG-----AA 807

Qy 832 CAGAAACGGAGCCGGAGCTGCACCAACCGCGCTCTCTCAACGGGGCGCTTTCTGTGAG 891

Db 808 CATTTGGGATCCGGGAGTGCACAGCACCAACCCCGAGAAATGGGGGCAAAATTTCTGTGA 867

Qy 892 GGGCAGAAATGTCCAGAAAAACAGCTGCGCCACCTGTGCCCCAGTAGAGCGAGCTGGAGC 951

Db 868 GGTCTAAGCCAGGAAATCTGAAAACTGCACAGATGGTCTTTGCACTCTTAGGCAATGAGA 927

Qy 952 CCGTGGAGCAAGTGGTGGGCTGTGGCTGAGCTGCACCCACTGGCGGAGCCGTGAGTGC 1011

Db 928 GCCAGCGACATTGCTTTGTACTCGGGCTTGG----- 958

Qy 1012 TCTGACCCAGCACCCCGAAACGAGGGGAGAGTGCAGGGGCACTGACCTGGACACCGCG 1071

Db 959 -----GTGCTGCGCTGCTGGCCGTTGCACTCTGGTCACTTGGTGTCACTTGGTGTCA 1002

Qy 1072 AACTGTACCATGACCTCTGTGTACACAGTCTTCTGGCCCTGAGGAGTGGCCCTCTAT 1131

Db 1003 CTTTACAGACGGAGCCAGAGTACTATGGCGTGAAGCTCAATTGACTCTTCTGCAATGACA 1062

Qy 1132 GTGGGCTCATCGCGGTGGCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1191

Db 1063 GGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGGTAACTCCCTGCTCTGNA 1122

Qy 1192 TATTGCCGGAAGAGAGGGGCTGGACTCAGATGTGGCTGACTGCTCAATCTTCACTCA 1251

Db 1123 TCTGCCATGCA-----GCCAGATCTGACAGTGAAGCGGACATACAGCGGAGCCATCT 1174

Qy 1252 GGTCTCCAGCCGCTCAGCATCAAGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1311

Db 1175 GTCTGACGAGCCCTCTGGACAAGG---AGCTCATGACAGAGTCTCTCACTCTTTAAACCT 1231

Qy 1312 CAGCGGACCTCAGCAGCACCAACCACTTACAGGGGAGTCTCTGCTCCCGGAGGAT 1371

Db 1232 TGTGGACATCAAGTGAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGA 1291

Qy 1372 GGGCCAGGCCCAAGTTCAGCTCACCAATGGGACCTGCTGAGCCCCCTGGGTGGCGGC 1431

Db 1292 GAGCTGAGTACCAACGAGGAGGAGTCAATTCAGGAGCTTT----- 1329

Qy 1432 GGGCAGACACTGCGACACAGCTCTCCACCTCTGAGGCGGAGGAGTTCGTTCCCGGCTC 1491

Db 1330 CCCATGGAACAAACACAGCTTTAGTACAAATGCAATGCCAGAAATAAAATGCCCTATAC 1389

Qy 1492 TCCACCCAGAACTACTTCCGCTCCCGGAGGACCAAGCAACATGACCTATGGGAGC 1551

Db 1390 CAAAATCTGT-----CATCACTCCCAAGGAGACAGTGAAGCACTGAGTGTG 1440

Qy 1552 TTCAACTTCTCGGGGCGCGCTGATCCCTTAATACAGGTATCAGCTCTCTCATCCCC 1611

Db 1441 TTTGGCCATTTAGGGGGCGCTTAGTAAAGCCAAATACAGGGGTGAGCTTACTCATACCA 1500

Qy 1612 CCAGATGCCATACCCGAGGAGAGTCTATGAGATCTACCTCAGCTGCAAGCCCGAA 1671

Db 1501 CAGGTGCCATCCAGAGGAGAAATCTTGGGAGATTTATATGTCAT---CAACCAAGGT 1557

Qy 1672 GAGTGAAGTGTGCGCTGAGTGTGAGACCTGCTGAGTCCCATCTGTAGTGTGGA 1731

Db 1558 GAACCCAGCTTCCAGTCAAGTGGCTCTGAGTGTCTGAGTCTTGAAGTCACTGTGTT 1617

Qy 1732 CCCCTGCGCTCTGCTCAGCCCGGCGAGTCACTCTGGCTATGAGACCACTGTGGGGAGCC 1791

Db 1618 CTTCCAGACATGATCGTCAACCACTCCCTTTGCACTGACCATCCGCACTGTGCAAGTGT 1677

Qy 1792 AGCCCTGACAGCTGGAGGCTGCGCTCAAAAGACAGTGTGCGGAGGAGGAGTGGAGGAT 1851

Db 1678 AGTTCTGAGCATTTGGAATATCCATTTAAAGAGAGAGACAGCAGGGGCAATGGAGGAA 1737

Qy 1852 GTCTGCACTGCGGAGGAGGCGCTCCCACTCTACTACTCTGAGCTGAGGAGGAGGAGG 1911

Db 1738 GTGATGTCAGTGAAGATGATCTATCATC-----CTGTTACTGCTTTTGGACCCCTTT 1791

Qy 1912 GCCTGCTAGTCTTCAACCGAGAGCTGGGGCGCTTTGCGCTGTGGGAGAGGCGCTCAGC 1971

Db 709 TCACTCCCCACAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGC 768
Qy 1573 CTGATGATCCCTAATACAGGTATCAGCTCTCATCCCCCAGATGCCATACCCGAGGG 1632
Db 769 TTAGTAATGCCAATACAGGGGTGAGTTACTCATACACAGGTGCCATCCACAGAGAG 828
Qy 1633 AAGATCTATGAGATCTACCTCAGCTGCACAAAGCCGGAAGACGTGAGGTTGCCCTAGCT 1692
Db 829 AATTCCTTTGGGAGATTTATATGTCCATCAACAAGGTGAACCC---AGCCTCCAGTCAGAT 885
Qy 1693 GGCTGTGAGACCCCTGTGAGTCCATCGTTAGCTGTGGACCCCTGTGGCTCTGCTCAAC 1752
Db 886 GGCTGTGAGTGTCTGTGAGTCTGAAAGTCACTGTGTCTCTCCAGACATGATGTCACC 945
Qy 1753 CGGCAGTCTATCGGTATGACCACTGTGGGAGCCAGCCCTGACAGCTGACAGCTGAGCCTG 1812
Db 946 ACTCCCTTTGCAATGACATCCCGCATGTGCAGATGTAGTCTGAGCATTTGGAATATC 1005
Qy 1913 CGCTCAAAAAGCAGTCTGCGAGGGCAGCTGGGAGGATGTCTGCAACCTGGGCGAGGAG 1872
Db 1006 CATTTAAAGAGAGGACACAGCAGGGCAATGGGAGGAGTGTCTCAGTGGGAAGTAA 1065
Qy 1873 GCGCCCTCCACCTCTACTACTGTCAGCTGAGGCCAGTGTGCTGTAGCTCTTACCGAG 1932
Db 1066 TCTACATC-----CTGTTACTGCTTTTGGACCCCTTTGGCTGTCTATGTGCTCCTGGAC 1119
Qy 1933 CAGCTGGGCGCTTTGCTGCTGGGAGAGCCCTCAGCTGTGGCTGCGCCAGAGCGCTC 1992
Db 1120 AGCTTTGGGACCTATGCGCTCACTGGAGAGCAATCAACAGCTGTGCGCGTGAAGCAACTG 1179
Qy 1993 AAGCTGCTTCTGTTTGGCGCGGTGCTGCACTCCCTCGAGTACAACTCCGGGTCTAC 2052
Db 1180 AAGTGGCGGTTTGGCTGATGTCTGTAACTCCCTGGATTAACATTTGAGAGTTTAC 1239
Qy 2053 TGGCTGATGACACCCACAGATGCACTCAAGAGGTGTGTGAGCTGTGAGAGAGAGCTGGG 2112
Db 1240 TGTGTGACAAATACCCCTTGTGCAATTTCAAGAAAGTGTGTTTTCAGATGAAGGCATCAAGGT 1299
Qy 2113 GGAAGCTGATCCAGGAGCAGCGGTCTGCACTTCAAGGACAGTTTACCAACACTGCGC 2172
Db 1300 GGAAGCTCTGGAAGAACAAATTTGCTGCAATTTCAAGGAAATACCTTTAGTCTTTAG 1359
Qy 2173 CTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCTTGTGAGTACCAAG 2232
Db 1360 ATTTCTGCTCTGATATTCGCCCATTCCTCTGGAGATTAACCACTTCACTGCTGCCAG 1419
Qy 2233 GAGATCCCTTTTATCACTCTGGAATGGCAGCGGGTACTTGTGACTGCACTTCAAC 2292
Db 1420 GAAATCCCGTTCTCCCGCGTGTGTGCAATTAACCGGAGCCCTTGCACTGTGCTTCTCC 1479
Qy 2293 CTGGAGGCTGTGAGCCCGAGCACTAGTGACCTGCGCTGCAAGCTGTGGGTGTGCGAGTG 2352
Db 1480 CTGAGGGTTATAGCCCACTACCCAGCTGTCTGCAAAATCTGCAATTCGCGAGCTC 1539
Qy 2353 GAGGGCAGCGGAGAGCTTTCAGCATCAACTTCAACATCAAGGACACAAAGTTTGCT 2412
Db 1540 AAGGCCATGAACAGATCTCTCAAGTCGACATCAATCTAGAGAGTGAAGAGAAACC 1599
Qy 2413 GAGCTGTGCTGTGAGAGTGAAGCGGGGTCTCAGCCCTGTGGGCCCGCCAGTGCCTTC 2472
Db 1600 ATCACTTTCTTCGCAAGAGGACAGCACTTTCCTGCAAGAGCTGGCCCCCAAGCCTTC 1659
Qy 2473 AAGATCCCTTCTCATTCGCGCAAGATTAATTTCCAGCTGAGCCAGCCCTGTAGCGG 2532
Db 1660 AAAATTCCTACTCATCAGACAGGGAATTTGTGCTACATTTGATACCCCAATGCAAA 1719
Qy 2533 GGTGCCAGCTGGCGGACTCTGGCCAGAAAATCTCACCCTGGACAGCAATCTCAGCTTCTTT 2592
Db 1720 GGCAGAGACTGGCAGATGTTAGACAGAAAACAGCATCAACAGGAATTTATCTTATTC 1779
Qy 2593 GCCTCAAGCCAGCCCAAGCCATGATCTCAACTGTGGAGGCGGCGCACTTCCCC 2652
Db 1780 GCTACACAAAGTAGCCCATCTGCTGTCAATTTTGAACCTGTGGGAGCTGCTCATCAGCAT 1839

Qy 2653 AACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGAGCTGGGCCAGACGCTGGC 2712
Db 1840 GATGGTGAATCTTGAATCTCCCTGGCTGTGCCCTTGAAGAGATTTGGAGGACACACACGAAA 1899
Qy 2713 CTCTTCAACAGTGTCCGAGGCTGAG 2736
Db 1900 CTCTCAACATTTTCAAGTCCAG 1923

RESULT 15

US-09-969-532-29
; Sequence 29, Application US/09969532
; Patent No. 677232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-29

Query Match 10.7%; Score 293.2; DB 4; Length 2001;
Best Local Similarity 53.7%; Pred. No. 5.8e-56;
Matches 657; Conservative 0; Mismatches 558; Indels 9; Gaps 2;

Qy 1513 TCCTGCCCGGAGCCAGCAACATGACCTATATGGACCTTCAACTTCTCGGGGCGCG 1572
Db 742 TCACTCCCAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGC 801
Qy 1573 CTGATCATCCCTAATACAGGTATCAGCTCTCATCCCCCAGATGCCATACCCGAGGG 1632
Db 802 TTAGTAATGCCAAATACAGGGTGAAGTTACTCATACCACAGGTGCCATCCCAAGAGAG 861
Qy 1633 AAGATCTATGAGATCTACCTCAGCTGCACAAAGCCGGAAGACGTGAGTTGCCCTAGCT 1692
Db 862 AATCTTGGAGATTTATATGTCTCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGAT 918
Qy 1693 GGCTGTGAGACCTCTGTGAGTCCCATCGTTAGTGTGGACCCCTGTGCTGCTCAAC 1752
Db 919 GGCTGTGAGTGTCTGTGAGTCTGAAAGTCACTGTGGTCTCCAGACATGATCGTCACC 978
Qy 1753 CGGCCAGTCACTCTGCTATGAGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCCTG 1812
Db 979 ACTCCCTTTGCAATTTGACCATCCCGCACTGTGCAAGATGTCTAGTCTGAGCATTTGAATATC 1038
Qy 1813 CGCCTCAAAAAGCAGTCTGTGCGAGGCGAGTGTGCTGCACCTGGCGAGGAG 1872
Db 1039 CATTTAAGAGAGGACACAGCAGGGCAATGGAGGAGTGTGATGTCAGTGGAAAGTAA 1098
Qy 1873 GCGCCCTCCCACTCTACTACTGCGAGCTGGAGGCCAGTGTGCTGTACTAGCTTTTCAACGAG 1932
Db 1099 TCTACATC-----CTGTTACTGCTTTTGGACCCCTTTTGGCTGTCTATGTGCTCTGGAC 1152
Qy 1933 CAGCTGGGCGCTTTTCCCTGTGGGAGAGGCCCTCAGCGTGGCTGCCCGCAAGCGCTC 1992
Db 1153 AGCTTTGGGACCTTATGCTCACTGGAGAGCCCAATCAAGATGTGTGCCGTGAAGCAACTG 1212
Qy 1993 AAGCTCTCTTCTTGTTCGCGCGGTGGCTGCACTCTCGAGTACAACTCCGGGTCTAC 2052
Db 1213 AAGTGGCGGTTTTTGGCTGATGTCTGTAACTCCCTGGAATTTACAACTTGAGAGTTTAC 1272
Qy 2053 TGCTCTGATGACACCCAGCATGCACTCAAGGAGGTGTGCAAGCTGGAGAGAGCAGCTGGG 2112

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Db 1273 TGTGTGACAAATACCCCTTGTGCAATTTCAAGAGTGGTTTCAGATGAAGGCAATCAAGGT 1332
Qy 2113 GGAAGAGTGAATCCAGGAGCAACGGGTCCTGCACCTTCAAGGACAGTTATACCAACACCTGCGC 2172
Db 1333 GGAAGAGTCCCTGGGAAGAACCAAAATGCTGCAATTTCAAGGGAATACCTTTAGTCTTTCAG 1392
Qy 2173 CTATCCATCCACGATGCGCCAGCTCCCTGTGGAGAGTAAGCTCCTTGTGTCAGTACCAG 2232
Db 1393 ATTTCTGTCTTGATATTCGCCCAATTCCTCTGGAGAAATTAACCAATTCACGTGCTGCCAG 1452
Qy 2233 GAGATCCCTTTTATACATCTTGAATGGCAGCGGGTACTTGCACCTGCACCTTCACC 2292
Db 1453 GAAGTCCCGTTCTCCCGGTGTGTGCAGTAACCGGAGCGCCCTGCACCTGTGCTTCTCC 1512
Qy 2293 CTGAGAGGTGTGACCCCGACAGCACTAGTGAACCTGGCCCTGCAAGCTGTGGGTGTGGCAGGTG 2352
Db 1513 CTGAGAGGTATATAGCCCACTACCCAGCTGTCTGCAAAATCTGCAATTCGCAGCTC 1572
Qy 2353 GAGGCGACGGGAGAGCTTCAGCATCACTTCAACATCACCAGGACACAAGTTTGCT 2412
Db 1573 AAGGCCATGAACAGATCTCCAAAGTGCAGACATCAATCTAGAGAGTGAACGAGAAACC 1632
Qy 2413 GAGCTGTGCTCTGGAGAGTGAAGCGGGGTCCAGCCCTGTGGGCCCGCAGTGCCTTC 2472
Db 1633 ATCACTTTCTTGGACAAAGAGGACAGCACTTCCCTGCACAGACTGGCCCCCAAGCCTTC 1692
Qy 2473 AAGATCCCTTCTCTCATTTGGCGAGAGATTAATTTCCAGCCCTGGACCCACCCTGTAGGGCGG 2532
Db 1693 AAAATTCCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCAATGCCAAA 1752
Qy 2533 GGTGCCAGCTGGGGACTCTGGCCCGAGAACTCCACCTGGACAGCCATCTCAGCTTCTTT 2592
Db 1753 GGCAGGACTGGCGAGATGTTAGCACAGAAAACAGCATCAACAGGAATTTATCTTATTTT 1812
Qy 2593 GCCTCCAAAGCCAGCCCCACAGCCATCATCTCAACCTGTGGAGGCGCGCACCTTCCCC 2652
Db 1813 GCTACACAAAGTAGCCCATCTGCTGTCTATTTTGAACCTGTGGAGAGCTCGTCATCAGCAT 1872
Qy 2653 AAGGGCAACCTCAGCCAGCTGGGTGACAGAGTGGCTGGACTGGGCCAGCCAGACGCTGGC 2712
Db 1873 GATGGTGATCTTGACTCCCTGGCCCTGTGCCCTTGAAGAGATTTGGGAGGACACACAGAAA 1932
Qy 2713 CTCTTACAGTGTGGAGGCTGAG 2736
Db 1933 CTCTCAAAACATTCAGAAATCCAG 1956
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Search completed: August 7, 2005, 22:31:21
Job time : 647 secs


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; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-779-1

Query Match      100.0%; Score 2752; DB 10; Length 2752;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCGGGGGCCCGCGCCGCGCGCCCGCGCCCGCGCGCCCGCGCGCCCGCGCGCCCGCGCGCC 60
Db 1 CCGCGGGGGCCCGCGCCGCGCGCCCGCGCCCGCGCGCCCGCGCGCCCGCGCGCCCGCGCGCC 60

Qy 61 GGCGTGTGGCGAGCGCTCTTGGGCATAGTCTTGGCGCGTGGCTTGGCTTGGCTTGGCTTGG 120
Db 61 GGCGTGTGGCGAGCGCTCTTGGGCATAGTCTTGGCGCGTGGCTTGGCTTGGCTTGGCTTGG 120

Qy 121 CAGCAGAGTGCACCGTGGGCCAACCCAGTGCCTGGTGCACCCGAGACCTGCTTCCCGCAC 180
Db 121 CAGCAGAGTGCACCGTGGGCCAACCCAGTGCCTGGTGCACCCGAGACCTGCTTCCCGCAC 180

Qy 181 TTCTGTGTGGAGCCGAGGATGTATCATCGTCAAGAAACAGCCAGTGTCTTGTGTGC 240
Db 181 TTCTGTGTGGAGCCGAGGATGTATCATCGTCAAGAAACAGCCAGTGTCTTGTGTGC 240

Qy 241 AAGCCGTGCGCGCACGCGATCTTCTTCAAGTGCMAACGGGAGTGGGTGGCGCAGGTG 300
Db 241 AAGCCGTGCGCGCACGCGATCTTCTTCAAGTGCMAACGGGAGTGGGTGGCGCAGGTG 300

Qy 301 GACCAGTGTATCAGCGCAGCAGCAGCAGCGGAGCGTGGGCTGCCACCAAGAGAGTCCGC 360
Db 301 GACCAGTGTATCAGCGCAGCAGCAGCAGCGGAGCGTGGGCTGCCACCAAGAGAGTCCGC 360

Qy 361 ATTAATGTCTCAAGGCGAGCGAGTGCAGAGAGTGTTCGGGCTGGAGGAATATCTGGTCCAG 420
Db 361 ATTAATGTCTCAAGGCGAGCGAGTGCAGAGAGTGTTCGGGCTGGAGGAATATCTGGTCCAG 420

Qy 421 TGGGTGCATGAGACTCTCGGGCACCAACAGAGTGCAGAGGCTTACATCCCGATAGCC 480
Db 421 TGGGTGCATGAGACTCTCGGGCACCAACAGAGTGCAGAGGCTTACATCCCGATAGCC 480

Qy 481 AGATTGGCAAGAACTTCGAGCAGGAGCCGCTGSCCAAGAGAGTGTCCCTGGAGCAGGGC 540
Db 481 AGATTGGCAAGAACTTCGAGCAGGAGCCGCTGSCCAAGAGAGTGTCCCTGGAGCAGGGC 540

Qy 541 ATCGTGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGTGGAGTGGCTCCGG 600
Db 541 ATCGTGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGTGGAGTGGCTCCGG 600
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Qy 601 AACGAGGACCTGTGTGGACCCGTCCTTGGACCCCAATGTATATCATCACGCGGAGCAGC 660
Db 601 AACGAGGACCTGTGTGGACCCGTCCTTGGACCCCAATGTATATCATCACGCGGAGCAGC 660

Qy 661 CTGGTGGTGAGCAGGCGCGCTTGTGTGACACGGCCAACTACACCTGCGTGGCCAAAGAC 720
Db 661 CTGGTGGTGAGCAGGCGCGCTTGTGTGACACGGCCAACTACACCTGCGTGGCCAAAGAC 720

Qy 721 ATCGTGGCAGCTCGCGCAGCGCTCCGCTGTGTATCGCTACGTGAACCGTGGGTGG 780
Db 721 ATCGTGGCAGCTCGCGCAGCGCTCCGCTGTGTATCGCTACGTGAACCGTGGGTGG 780

Qy 781 TCACGCTGGACCGAGTGGTCCGCTGTGACGCGCAGCTGTGGGCGCGCTGGCAAAACGG 840
Db 781 TCACGCTGGACCGAGTGGTCCGCTGTGACGCGCAGCTGTGGGCGCGCTGGCAAAACGG 840

Qy 841 AGCGGGAGCTGCACCAACCCGCGCGCTCTCAACGGGGGGCGCTTCTGTGAGGGGCGAGAT 900
Db 841 AGCGGGAGCTGCACCAACCCGCGCGCTCTCAACGGGGGGCGCTTCTGTGAGGGGCGAGAT 900

Qy 901 GTCCAGAAACAGCCTGCGCCACCCCTGTGCCAGTAGACGCGCAGCTGGAGCCCGTGGAGC 960
Db 901 GTCCAGAAACAGCCTGCGCCACCCCTGTGCCAGTAGACGCGCAGCTGGAGCCCGTGGAGC 960

Qy 961 AAGTGTGGGCTGTGGGTGGAGTGCACCCACTGGCGGAGCGCTGAGTGTCTGTGACCCA 1020
Db 961 AAGTGTGGGCTGTGGGTGGAGTGCACCCACTGGCGGAGCGCTGAGTGTCTGTGACCCA 1020

Qy 1021 GCACCCGCGCAACGGAGGGAGTGCACGGGCACTGACCTGCAGCACCCCGCACTGTACC 1080
Db 1021 GCACCCGCGCAACGGAGGGAGTGCACGGGCACTGACCTGCAGCACCCCGCACTGTACC 1080

Qy 1081 AGTGACCTCTGTGTACACAGTCTTCTGGCCCTGAGGACGCTGGCCCTCTATGTGGGCTC 1140
Db 1081 AGTGACCTCTGTGTACACAGTCTTCTGGCCCTGAGGACGCTGGCCCTCTATGTGGGCTC 1140

Qy 1141 ATCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1200
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Qy 1201 AAGAAAGGGGGCTGACCTAGATGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
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Qy 1261 CCGGTGAGCATCAAGCCAGCAAGCAGCAACCCCATCTGCTCACCATCCAGCCGGAC 1320
Db 1261 CCGGTGAGCATCAAGCCAGCAAGCAGCAACCCCATCTGCTCACCATCCAGCCGGAC 1320

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Db 1321 CTGAGCACACACACACACACCTACAGGGGAGTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1380

Qy 1381 CCCAAGTTCAGCTCACCAATGGGCACTGCTCAGGCCCCCTGGGTGGCGCGCCACACA 1440
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Qy 1441 CTGCACACAGCTTCCCACTCTGAGGCGGAGGAGTGTGCTCTCCGCTCTCCACCCAG 1500
Db 1441 CTGCACACAGCTTCCCACTCTGAGGCGGAGGAGTGTGCTCTCCGCTCTCCACCCAG 1500

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Qy 1561 CTGGGGGGCGGCTGATGATCCCTAATACAGGTATCAGGCTCTCTCATCCCCCAGATGCC 1620
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Qy 1621 ATACCCCGAGGGAAGATCTATGATCTACCTCACTGCAAGCCGGAAGAGCTGAGG 1680
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1861 CTGGGCGAGAGGCGCCCTCCCACTTACTACTGCTGAGGCGAGCTGAGGCGAGCTGAGGCGCTGCTAC 1920
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1921 GTCTTACCGAGAGCTGGGGCGCTTTTGGCGCGGTGCGCTGCACTCCCTCGAGTACAAC 1980
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1981 GCCAAGCGCCTCAAGCTGCTTCTGTTGGCGCGGTGCGCTGCACTCCCTCGAGTACAAC 2040
1981 GCCAAGCGCCTCAAGCTGCTTCTGTTGGCGCGGTGCGCTGCACTCCCTCGAGTACAAC 2040
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2041 ATCCGGGTCTACTGCTGCTATGACACCCAGATGCACTCAAGGAGGTGCTGCACTGGAG 2100
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2101 AAGCAGCTGGGGGACAGCTGATCAGAGGCGCCAGGCTCTGCACTTCAAGGACAGTTAC 2160
2161 CACAACCTGGCGCTTATCCATCCAGAGTGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTT 2220
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2221 GTCACTACCAAGAGATCCCTTTTATCACAATCTGGAATGGCAGCGGTACTTGCAC 2280
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2281 TGCACCTTACCTTGAAGAGTGTGAGCCGAGCTAGTACCTGGCTGGCTGCAAGCTGTGG 2340
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2341 GTGTGGCAGTGTGAGGCGGAGCGGAGCTTCAAGCTCAACTTCAACATCACCAGGAC 2400
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2401 ACAAGGTTTGTGAGCTGTGGCTCTGAGAGTGAAGCGGGGTGCCAGCCCTGGTGGGC 2460
2401 ACAAGGTTTGTGAGCTGTGGCTCTGAGAGTGAAGCGGGGTGCCAGCCCTGGTGGGC 2460
2461 CCAGTGCCTTCAAGATCCCTTCTCTCAATTCGGCAGAGATAATTTCCAGCTGGAGCCCA 2520
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2521 CCCTGTAGGGGGGTGCGGAGCTGCGGACTTGTGCCAGAGAACTCCACCTGGACAGCCAT 2580
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2581 CTCAAGCTTCTTGTGCTTCAAGCCAGCCAGCCAGCTATGATCTCTCAACCTGTGGAGGCG 2640
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2641 CGGCACTTCCCAACGGCAACCTCAGCAGCTGCTGAGGAGTGGCTGAGCTGGGCGAG 2700
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RESULT 2
US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication NO. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shinkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-624-932-1

Query Match 100.0%; Score 2752; DB 18; Length 2752;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGCGGGGCCCCCGCCCGCCCGCTGCGCCCGCGGCGCATGGCGCTCCGGGCC 60
DB 1 CCAGCGGGGCCCCCGCCCGCCCGCTGCGCCCGCGGCGCATGGCGCTCCGGGCC 60
QY 61 GGCTGTGGCCAGCGCTCTTGGGCATAGTCTTCCCGCTTGGCTCCGCGCTGGGTGCC 120
DB 61 GGCTGTGGCCAGCGCTCTTGGGCATAGTCTTCCCGCTTGGCTCCGCGCTGGGTGCC 120
QY 121 CAGCAGAGTGCCACCGCTGGGCAACCCAGTGCCTTGGTGCACCCGAGACCTGCTTCCCAC 180
DB 121 CAGCAGAGTGCCACCGCTGGGCAACCCAGTGCCTTGGTGCACCCGAGACCTGCTTCCCAC 180

Qy		181	TTCCTGTTGGAGCCCGAGGAATGTGTA CATCGTCAAGAAACAAGCAGTGCTGCTTGTGTGC	240
Db		181		
		181	TTCCTGTTGGAGCCCGAGGAATGTGTA CATCGTCAAGAAACAAGCAGTGCTGCTTGTGTGC	240
Qy		241	AAGGCCGTGCCCGCACGCGAATCTTCTTAAGTGC AACGGGNGTGGTGCCCGCAGGTG	300
Db		241		
Qy		301	GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCAACATGGAGGTCCGC	360
Db		301		
Qy		361	ATTAAATGTCTCAAGGACAGAGGTCGAGAAGGTGTTCCGGCTGGAGGAATACTGGTGCAG	420
Db		361		
Qy		421	TGCGTGGCNTGGAGCTCCTCGGCGACCAACNAGAGTCAG AAGGCTACATCCGCATAGCC	480
Db		421		
Qy		481	AGATTGGCCAAGAACTTCGAGCAGCAGCGCTGGCCCAAGGAGTGTCCCCTGGAGCAGGGC	540
Db		481		
Qy		541	ATCGTGTGCCCTCGCGTCCAACGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	600
Db		541		
Qy		601	AACGAGGACTGGTGGACCCGTCCCTGGACCCCAATGTATACATCAGCGGGAGCACA GCG	660
Db		601		
Qy		661	CTGTTGTTGGACAGSGCCGCGCTTCTGTGACACGSCCACTACACCTCGGTGGCCCCAGAAC	720
Db		661		
Qy		721	ATCGTGGCAGCTCGCCGAGCGCCTCCGCTGCTCATCGTCTACGTGAACGGTGGGTGG	780
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Qy		781	TCGACGTGGACCGAGTGGTTCGTTGACAGCGC CAGCTGTGGGCGCGGCTGGCAGAAA CGG	840
Db		781		
Qy		841	AGCCGAGCTGCACCAACCCGGCCCTCTCAAACGGGGCGCTTCTCTGTGAGGGGCGAGAAT	900
Db		841		
Qy		901	GTCAGAAAAACAGCTCGCGCACCTGTGCCAGTAGACGCGCAGCTGGAGCCCGTGGAGC	960
Db		901		
Qy		961	AAGTGTGCGGCTGTGGGCTGGAC TGGACACCA CTGGCGGAGCCGTGAGTGTCTGACCCCA	1020
Db		961		
Qy		1021	GCA CCCCGAACGAGAGGGAGGTGCCAGGCACTGACCTGGACACCCGCACTGTACC	1080
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Qy		1081	AGTGACCTCTGTGTACAGTGTCTCTGGCCCTCAGGACGTGGGCCCTCTATGTGGGCTC	1140
Db		1081		
Qy		1141	ATCGCGTGGCCGTCTGCTGGTCCCTGTGCTTGTCTCATCTCTCGTTTATGTCCGG	1200
Db		1141		
Qy		1201	AAG AAGAGGGGCTGGACTAGATGCTGGCTGACTCTGCTCAATCTCTCACTCAGGCTTCAG	1260
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1261	Db		CCCGTCAGCATCAAGGCCAGCAAAAGCAGACAACCCCCATCTGCTCAACCTCCAGCCGGAC	1320
1321	Qy		CTCAGCACCAACACACCACTACCAAGGCGAGTCTGTGCCCGGCGAGATGGGCCCCAGC	1380
1321	Db		CTCAGCACCAACACACCACTACCAAGGCGAGTCTGTGCCCGGCGAGATGGGCCCCAGC	1380
1381	Qy		CCCAAGTTCCAGCTCACCAATGGGCACTGCTCAGCCCCCTGGGTGGCGCGCCACACA	1440
1381	Db		CCCAAGTTCCAGCTCACCAATGGGCACTGCTCAGCCCCCTGGGTGGCGCGCCACACA	1440
1441	Qy		CTGGACCAAGCTCTCCACCTCTGAGGGCGAGGATTGTTCTCCGCTCTCCACCCAG	1500
1441	Db		CTGCACCAAGCTCTCCACCTCTGAGGGCGAGGATTGTTCTCCGCTCTCCACCCAG	1500
1501	Qy		AATCTCTTCGGCTCCCTGCCCGGAGCACCGACAATGACCTTATGGGACCTTCAACTTC	1560
1501	Db		AATCTCTTCGGCTCCCTGCCCGGAGCACCGACAATGACCTTATGGGACCTTCAACTTC	1560
1561	Qy		CTCGGGGGCGGCTGATGATCCCTAATACAGGTATCAGGCTCTCTATCCCCCAGATGCC	1620
1561	Db		CTCGGGGGCGGCTGATGATCCCTAATACAGGTATCAGGCTCTCTATCCCCCAGATGCC	1620
1621	Qy		ATACCCCGAGGGAAGATCTATGAGATCTACTCA CGCTGCA CAAGCCGGAAGACGTGAGG	1680
1621	Db		ATACCCCGAGGGAAGATCTATGAGATCTACTCA CGCTGCA CAAGCCGGAAGACGTGAGG	1680
1681	Qy		TTGGCCCTAGCTGGCTGCAGACCTCTGAGTCCCATGTTAGCTGTGGACCCCTGGC	1740
1681	Db		TTGGCCCTAGCTGGCTGCAGACCTCTGAGTCCCATGTTAGCTGTGGACCCCTGGC	1740
1741	Qy		GTCTGTCTACCCGGCGCAGTCATCTCGGCTATGGACCACTGTGGGAGGCCACGCCCTGAC	1800
1741	Db		GTCTGTCTACCCGGCGCAGTCATCTCGGCTATGGACCACTGTGGGAGGCCACGCCCTGAC	1800
1801	Qy		AGCTGGAGCTCGCCTCAAAAAGCAGTCTGTGGAGGGCAGCTGGGAGGATGTGTGCA	1860
1801	Db		AGCTGGAGCTCGCCTCAAAAAGCAGTCTGTGGAGGGCAGCTGGGAGGATGTGTGCA	1860
1861	Qy		CTGGGCGAGGAGGGCCCTCCACCTCTACTACTGCTGCACTGGAGGCCAGTGCCTGTAC	1920
1861	Db		CTGGGCGAGGAGGGCCCTCCACCTCTACTACTGCTGCACTGGAGGCCAGTGCCTGTAC	1920
1921	Qy		GTCTTACCCAGCAGCTGGGCGCCTTTGGCTGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
1921	Db		GTCTTACCCAGCAGCTGGGCGCCTTTGGCTGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
1981	Qy		GCCAAAGCCCTCAAGTGTCTTTTGGCGCGGTGGCCTTGCACTTCTCGAGTACAAC	2040
1981	Db		GCCAAAGCCCTCAAGTGTCTTTTGGCGCGGTGGCCTTGCACTTCTCGAGTACAAC	2040
2041	Qy		ATCGGGTCTACTGCTGTGATGACACCCAGATGCACTCAAGGAGTGTGCACTGGAG	2100
2041	Db		ATCGGGTCTACTGCTGTGATGACACCCAGATGCACTCAAGGAGTGTGCACTGGAG	2100
2101	Qy		AAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCTGTCACTTCAAGGACAGTTAC	2160
2101	Db		AAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCTGTCACTTCAAGGACAGTTAC	2160
2161	Qy		CACAACCTGGCCTATCCATCCAAGATGTGCCAGTCTCCTGTGGAGAGTAACTCCTT	2220
2161	Db		CACAACCTGGCCTATCCATCCAAGATGTGCCAGTCTCCTGTGGAGAGTAACTCCTT	2220
2221	Qy		GTGAGTACAGAGATCCCTTTTATCACTGTGAATGGCACGCAAGCGGTACTTGCAC	2280
2221	Db		GTGAGTACAGAGATCCCTTTTATCACTGTGAATGGCACGCAAGCGGTACTTGCAC	2280
2281	Qy		TGCACCTTACCCCTGGAGGCTGTACGCCAGCACTAGTGAAGCTGCTGCTGCAAGCTGTGG	2340
2281	Db		TGCACCTTACCCCTGGAGGCTGTACGCCAGCACTAGTGAAGCTGCTGCTGCAAGCTGTGG	2340
2341	Qy		GTGTGGCAGGTGGAGGGCGACGGGCAAGGCTTTCAGCATCAACTTCAACATCAACAGGAC	2400

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2641 CGGCACCTTCCCAACGGCAACTCAGCCAGCTGCGCAGTGGCTGCGAGTGGGCGAG 2700
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2701 CCAGACGCTGGCCTTTCACAGTGTGCGAGGCTGAGTGTGAGCGCGGCCAG 2752
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2701 CCAGACGCTGGCCTTTCACAGTGTGCGAGGCTGAGTGTGAGCGCGGCCAG 2752

RESULT 3
US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Heriman, John L
; APPLICANT: Restelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; PRIOR FILING DATE: 2002-05-02
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

Query Match 97.3%; Score 2676.4; DB 10; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;
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Db 42 CCGGGGGCCCGCGCCCGCGCCCTGCGCCGCGCGGCGCATGGCGCC 101
Qy 61 GGCCTGTGGCAGCGCTCTGGGAGATAGTCTGCGCCGCTGGCTGCGCGGCTGGGTGCG 120
Db 102 GGCCTGTGGCAGCGCTCTGGGAGATAGTCTGCGCCGCTGGGTGCGCGGCTGGGTGCG 161
Qy 121 CAGCAGATGCCACCGTGGCCCAACCCAGTGGTGGCCCAACCCGACCTGCTTCCCCAC 180
Db 162 CAGCAGATGCCACCGTGGCCCAACCCAGTGGTGGCCCAACCCGACCTGCTTCCCCAC 221
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Db 342 GACCACTGATCGAGCCGACAGACGGGAGCAGTGGTGGTGGTGGTGGTGGTGGTGG 401
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Qy 421 TGGTGGCATGGAGCTCTCGGGCACCAAGAGTGTGAGAGGCTTACATCCGATAGCC 480
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Db 522 AGATTGGCGAAGAACTTCGAGAGGAGCGCTGCGGAGGAGTGTCCCTGGACGAGGC 581
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Db 822 TCAGAGTGTGACAGGAGTGTGCTGTGACGCGCAGCTGTGGGCGCGCTGGCAAGAACGG 881
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Db 1062 CCAGCACCCCGCAACCGAGGGAGGAGTGTGCGGCGCTGAGGAGCAGTGGCCCTCTATGTGGGC 1121
Qy 1078 ACCAGTGAACCTCTGTGTACACAGTGTCTGTGGCCCTGAGGAGCAGTGGCCCTCTATGTGGGC 1137
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Qy 1138 CTATGCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1197
Db 1182 CTATGCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1241
Qy 1198 CGGAAGAGAGGGGCTGGAGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
Db 1242 CGGAAGAGAGGGGCTGGAGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
Qy 1258 CAGCCGCTCAGCATCAAGCCGACCAAGAGCAGACAAACCCCATCTGTCTCAGCATCCAGCCG 1317
Db 1302 CAGCCGCTCAGCATCAAGCCGACCAAGAGCAGACAAACCCCATCTGTCTCAGCATCCAGCCG 1361
Qy 1318 GACCTCAGCACCAACACCACTACAGGAGGAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377
Db 1362 GACCTCAG---CACCAACCAACCTACAGGAGGAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1418

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Db 1479 AACTGACACACAGCTCTCCACCTCTGAGGCCGAGAGTTGCTCTCCGCTCTCCACC 1538
QY 1498 CAGAACTACTTCCGCTCCCTGCCCCGAGGACCAAGCAACATGACCTTATGGGACCTTCAAC 1557
Db 1539 CAGAACTACTTCCGCTCCCTGCCCCGAGGACCAAGCAACATGACCTTATGGGACCTTCAAC 1598
QY 1558 TTCTTCGGGGCGGCTGATGATCCCTTAATACAGGTATCAGCTCTCCTCATCCCCCAGAT 1617
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QY 1618 GCATATACCCGAGGGAAGATCTATGAGATCTACTCTCAGCTGCACAAGCCGGAAGAGCTG 1677
Db 1659 GCATATACCCGAGGGAAGATCTATGAGATCTACTCTCAGCTGCACAAGCCGGAAGAGCTG 1718
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Db 1719 AGFTTGCCCTAGTGTGCTGTACAGACCTGCTGAGTCCCCATCGTTAGCTGTGGACCCCT 1778
QY 1738 GCGTCTGCTCACCCGGCCAGTCTCTGCTATGACCACTGTGGGGAGCCAGCCCT 1797
Db 1779 GCGTCTGCTCACCCGGCCAGTCTCTGCTATGACCACTGTGGGGAGCCAGCCCT 1838
QY 1798 GACAGCTGGAGCCCTGCGCCTCAAAAGACGTCGTCGAGGGCAGCTGGG--AGGATGTG 1854
Db 1839 GACAGCTGGAGCCCTGCGCCTCAAAAGACGTCGTCGAGGGCAGCTGGGAGCAGATGTG 1898
QY 1855 CTGCACTGGGGGAGGAGGCGCCCTCCCACTTACTTACTGCGAGCTGGAGGCGCAGTGCC 1914
Db 1899 CTGCACTGGGGGAGGAGGCGCCCTCCCACTTACTTACTGCGAGCTGGAGGCGCAGTGCC 1958
QY 1915 TGCTAGCTCTTCCAGGACGCTGGGCGCTTTGGCCCTGCTGGAGAGGCCCTCAGCGTG 1974
Db 1959 TGCTAGCTCTTCCAGGACGCTGGGCGCTTTGGCCCTGCTGGAGAGGCCCTCAGCGTG 2018
QY 1975 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGGCGCGTGGCCTGCACCTCCCTCGAG 2034
Db 2019 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGGCGCGTGGCCTGCACCTCCCTCGAG 2078
QY 2035 TACAACATCCGGGTCTACTGCTGCTATGACACCCACGATGCACTCAAGGAGGTGTGCGAG 2094
Db 2079 TACAACATCCGGGTCTACTGCTGCTATGACACCCACGATGCACTCAAGGAGGTGTGCGAG 2138
QY 2095 CTGGAGAAGCAGCTGGGGGACAGCTGATCCAGAGGCCAGGGTCTCTGCACTTCAAGGAC 2154
Db 2139 CTGGAGAAGCAGCTGGGGGACAGCTGATCCAGAGGCCAGGGTCTCTGCACTTCAAGGAC 2198
QY 2155 AGTTACCAACCTTCCGCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2214
Db 2199 AGTTACCAACCTTCCGCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2258
QY 2215 CTCTTGTGACTACAGAGATCCCTTTTATCACAATCTGGAATGSCACGACGCGGTAC 2274
Db 2259 CTCTTGTGACTACAGAGATCCCTTTTATCACAATCTGGAATGSCACGACGCGGTAC 2318
QY 2275 TTGCACATGCACTTCAACCTTGGAGCGTGTGAGCCCGAGCACTAGTGACCTGGCCTGCAAG 2334
Db 2319 TTGCACATGCACTTCAACCTTGGAGCGTGTGAGCCCGAGCACTAGTGACCTGGCCTGCAAG 2378
QY 2335 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTTCAGCATCACTTCAACATCACC 2394
Db 2379 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTTCAGCATCACTTCAACATCACC 2438
QY 2395 AAGGACACAAGGTTTGTGATGCTGTGGCTCTGGAGAGTGAAGGGGGTCCAGGCCCTG 2454
Db 2439 AAGGACACAAGGTTTGTGATGCTGTGGCTCTGGAGAGTGAAGGGGGTCCAGGCCCTG 2498
QY 2455 GTGGGGCCAGTGTCTTCAAGATCCCCTTCTCATTCCGGCAGAGAATAATTTCCAGGCTG 2514
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Db 2499 GTGGGGCCAGTGTCTTCAAGATCCCTTCTCATTCCGCGAGAGATAATTTCCAGCCTG 2558
QY 2515 GACCCACCTGTAGGGGGGTGCGACTTGGCGGACTTGGCCCGAGAACTCCACCTGGAC 2574
Db 2559 GACCCACCTGTAGGGGGGTGCGACTTGGCGGACTTGGCCCGAGAACTCCACCTGGAC 2618
QY 2575 AGCCATCTCAGCTTCTTTGCTCCAAAGCCAGCCGCCACAGCCATGATCTCTCAACCTGTG 2634
Db 2619 AGCCATCTCAGCTTCTTTGCTCCAAAGCCAGCCGCCACAGCCATGATCTCTCAACCTGTG 2678
QY 2635 GAGCGCGGCACTTCCCAACGCGACCTCAGCAGCTGGCTGCAGAGTGGCTGCACTG 2694
Db 2679 GAGCGCGGCACTTCCCAACGCGACCTCAGCAGCTGGCTGCAGAGTGGCTGCACTG 2738
QY 2695 GGCAGCAGACGCTGGCCTCTTACAGTGTCCGAGGCTGAGTGTGAGGCCGCCAC 2752
Db 2739 GGCAGCAGACGCTGGCCTCTTACAGTGTCCGAGGCTGAGTGTGAGGCCGCCAC 2796
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RESULT 4

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US-10-643-795A-77
; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-643-795A-77
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Query Match 85.6%; Score 2356; DB 20; Length 3561;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;

QY 43 GCATGGCGGTCCGGCCCGGCTGTGGCAGCGCTCTCTGGGCATAGTCTCGCGCGTGG 102
Db 1 GCATGGCGGTCCGGCCCGGCTGTGGCAGCGCTCTCTGGGCATAGTCTCGCGCGTGG 60
QY 103 CTCGGCGGTTCGGGTCCCGCAGAGTGCACCGTGCACCAACCCAGTCTGTGCGCAAC 162
Db 61 CTCGGCGGTTCGGGTCCCGCAGAGTGCACCGTGCACCAACCCAGTCTGTGCGCAAC 120
QY 163 CCGGACCTGTCTCCCACTTCTCTGGTGGAGCCCGGAGATGTGTACATCGTCAAGAACAG 222
Db 121 CCGGACCTGTCTCTCCCACTTCTCTGGTGGAGCCCGGAGATGTGTACATCGTCAAGAACAG 180
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Qy	223	CCAGTGTCTGTGTGCAAGCGCGTGC	CGCCACGACGAGATCTTCTCAAGTCAACGGG	282
Db	181	CCAGTGTCTGTGTGCAAGCGCGTGC	CGCCACGACGAGATCTTCTCAAGTCAACGGG	240
Qy	283	GAGTGGGTGCCAGGTGGACCAAGTAT	CGAGCGCAGACAGAGAGAGTGGGTG	342
Db	241	GAGTGGGTGCCAGGTGGACCAAGTAT	CGAGCGCAGACAGAGAGAGTGGGTG	300
Qy	343	CCACCAATGAGGTCCGCAATTAATGT	CTCAAGGACAGAGTTCGAGAGTTCGGGCTG	402
Db	301	CCACCAATGAGGTCCGCAATTAATGT	CTCAAGGACAGAGTTCGAGAGTTCGGGCTG	360
Qy	403	GAGGAATACTGGTGCAGTGGGCATG	AGAGTTCCTCGGACACCAAGAGTCAAGAG	462
Db	361	GAGGAATACTGGTGCAGTGGGCATG	AGAGTTCCTCGGACACCAAGAGTCAAGAG	420
Qy	463	GCCTACATCCGCATAGCCAGATTCG	CAAGAACTTCGAGCAGAGCGCTGGCCAGGAG	522
Db	421	GCCTACATCCGCATAGCCATGCTTA	TTTGGCAAGAACTTCGAGCAGAGCGCTGGCCAGGAG	480
Qy	523	GTGTCCCTGGAGAGGGCATGCTGCT	GCCTGCGGTCCACCGAGGGGATCCCTCCAGCC	582
Db	481	GTGTCCCTGGAGAGGGCATGCTGCT	GCCTGCGGTCCACCGAGGGGATCCCTCCAGCC	540
Qy	583	GAGGTGAGTGGTCCCGAACAGGAC	CTGGTGACCCGCTCCCTGGACCCCAATGTATAC	642
Db	541	GAGGTGAGTGGTCCCGAACAGGAC	CTGGTGACCCGCTCCCTGGACCCCAATGTATAC	600
Qy	643	ATCACGGGGAGCAGCCTGGTGGTGC	AGCAGAGCCCGCTTGTGACAGGGCAACTAC	702
Db	601	ATCACGGGGAGCAGCCTGGTGGTGC	AGCAGAGCCCGCTTGTGACAGGGCAACTAC	660
Qy	703	ACCTGCGTCCAGAACATCGTGGCAG	CGCGCAGCGCCTCGCTGCTGTCATCGTC	762
Db	661	ACCTGCGTCCAGAACATCGTGGCAG	CGCGCAGCGCCTCGCTGCTGTCATCGTC	720
Qy	763	TACGTGAACCGTGGTGGTGCAGCTG	GACACGAGTGGTCCGCTCTGACGGCGAGCTGGG	822
Db	721	TACGTG-----	-----	726
Qy	823	CGGGCTGGCAGAAACGGAGCTGCA	CCAAACCGCGGCTCTCAACGGGGGCGCT	882
Db	727	-----	-----	726
Qy	883	TTCTGTGAGGGGAGAAATGTCAGAA	AACAGCCTGCGCCACCCTGTGCCCAAGTAGACGC	942
Db	727	-----	-----GACGGC	732
Qy	943	AGCTGAGCCCGTGGAGCAAGTGGT	CGGCTGTGGGCTGGACTGCACCCCACTGGCGGAGC	1002
Db	733	AGCTGAGCCCGTGGAGCAAGTGGT	CGGCTGTGGGCTGGACTGCACCCCACTGGCGGAGC	792
Qy	1003	CGTGAAGTCTGTACCCAGACCCCG	CAACGGAGGGAGAGTGCAGGGCACTGACCTG	1062
Db	793	CGTGAAGTCTGTACCCAGACCCCG	CAACGGAGGGAGAGTGCAGGGCACTGACCTG	852
Qy	1063	GACACCCGCAACTGTACAGTGAAC	CTGTGTACACAGTGTCTTGGCCCTTGAGGAGCTG	1122
Db	853	GACACCCGCAACTGTACAGTGAAC	CTGTGTACACAGTGTCTTGGCCCTTGAGGAGCTG	912
Qy	1123	GCCCTCTATGTGGGCTCATCGCG	CGTGGCTGTGCTGTGCTGTGCTGCTC	1182
Db	913	GCCCTCTATGTGGGCTCATCGCG	CGTGGCTGTGCTGTGCTGTGCTGCTC	972
Qy	1183	ATCCTCTTTATTGCCGGAAGAGG	GGGCTGACCTCAGATGTGGTGAATGCTGCTCAAT	1242
Db	973	ATCCTCTTTATTGCCGGAAGAGG	GGGCTGACCTCAGATGTGGTGAATGCTGCTCAAT	1032
Qy	1243	CTCACCTCAGGCTTCCAGCCGCT	CAGCATCAGCCGACGAGCAGACCAACCCCATCTG	1302
Db	1033	CTCACCTCAGGCTTCCAGCCGCT	CAGCATCAGCCGACGAGCAGACCAACCCCATCTG	1092

Qy	1303	CTCACCTCAGCGGACCTCAGCA	CCACCACCACTACCAAGGCGAGTCTCTGTCCC	1362
Db	1093	CTCACCTCAGCGGACCTCAGCA	CCACCACCACTACCAAGGCGAGTCTCTGTCCC	1152
Qy	1363	CGGAGGATGGGCGCCAGCCCAAG	TTCCAGTCAACCAATGGGCACTCTGCTCAGGCCCTGT	1422
Db	1153	CGGAGGATGGGCGCCAGCCCAAG	TTCCAGTCAACCAATGGGCACTCTGCTCAGGCCCTGT	1212
Qy	1423	GGTGGGCGCGCCACACATGCA	CCACAGCTCTCCACCTCTGAGGGCGAGGATTCGTC	1482
Db	1213	GGTGGGCGCGCCACACATGCA	CCACAGCTCTCCACCTCTGAGGGCGAGGATTCGTC	1272
Qy	1483	TCCGCGCTCTCCACCCAGAACT	ACTTCCGCTCCCGAGGACACAGCAATGACC	1542
Db	1273	TCCGCGCTCTCCACCCAGAACT	ACTTCCGCTCCCGAGGACACAGCAATGACC	1332
Qy	1543	TATGGGACCTTCAACTTCTCG	GGGGCGGCTGATTCCTTAATAACAGGTATCAGGCTC	1602
Db	1333	TATGGGACCTTCAACTTCTCG	GGGGCGGCTGATTCCTTAATAACAGGTATCAGGCTC	1392
Qy	1603	CTCATCCCCCAGATACCCGAG	GGAAGATCTATGAGATCTACCTCAGCGCTGCAC	1662
Db	1393	CTCATCCCCCAGATACCCGAG	GGAAGATCTATGAGATCTACCTCAGCGCTGCAC	1452
Qy	1663	AAGCCGGAAGACGTGAGTTC	CGCCCTAGCTGGCTGTGAGACCTCTGCTGAGTCCCATCGTT	1722
Db	1453	AAGCCGGAAGACGTGAGTTC	CGCCCTAGCTGGCTGTGAGACCTCTGCTGAGTCCCATCGTT	1512
Qy	1723	AGCTGTGGAACCCCTGGGCT	CTGCTCACCCGGGCACTCATCTCTGGGTATGGAACACTGT	1782
Db	1513	AGCTGTGGAACCCCTGGGCT	CTGCTCACCCGGGCACTCATCTCTGGGTATGGAACACTGT	1572
Qy	1783	GGGAGCCACCGCTGACAGCT	GGAGCTCGGCTCAAAAGCAGTGTGTCGAGGGGAGC	1842
Db	1573	GGGAGCCACCGCTGACAGCT	GGAGCTCGGCTCAAAAGCAGTGTGTCGAGGGGAGC	1632
Qy	1843	TGGGAGATGTGCTGACCT	GGGCGAGGCGGCTCCACACCTCTACTGTCAGCTG	1902
Db	1633	TGGGAGATGTGCTGACCT	GGGCGAGGCGGCTCCACACCTCTACTGTCAGCTG	1692
Qy	1903	GAGGCCAGTCTGTACGTCTT	CAACGAGAGTGGGCGCTTTGCGCTTGTGGGAGAG	1962
Db	1693	GAGGCCAGTCTGTACGTCTT	CAACGAGAGTGGGCGCTTTGCGCTTGTGGGAGAG	1752
Qy	1963	GCCTCAGCTGTGCTCGCC	CAAGCGCTCTCTGTTGGCGGCTGGGCTGC	2022
Db	1753	GCCTCAGCTGTGCTCGCC	CAAGCGCTCTCTGTTGGCGGCTGGGCTGC	1812
Qy	2023	ACCTCCCTCGAGTACAACAT	CCCGGTCTACTGCTGTCATGACACCCACGATGCACTCAAG	2082
Db	1813	ACCTCCCTCGAGTACAACAT	CCCGGTCTACTGCTGTCATGACACCCACGATGCACTCAAG	1872
Qy	2083	GAGGTGTGAGCTGGAGAA	AGCAGCTGGGGGACAGCTGATCCAGAGACCAAGGGTCTGT	2142
Db	1873	GAGGTGTGAGCTGGAGAA	AGCAGCTGGGGGACAGCTGATCCAGAGACCAAGGGTCTGT	1932
Qy	2143	CACCTCAAGGACATGTTAC	CAACACCTTCCATCCAGATGTGCCAGCTCCCTG	2202
Db	1933	CACCTCAAGGACATGTTAC	CAACACCTTCCATCCAGATGTGCCAGCTCCCTG	1992
Qy	2203	TGGAAGATTAAGCTCTTGT	CAGCTAC CAGGAGATCCCTTTTATCATCTGGAATGGC	2262
Db	1993	TGGAAGATTAAGCTCTTGT	CAGCTAC CAGGAGATCCCTTTTATCATCTGGAATGGC	2052
Qy	2263	ACGAGGGGTACTTGCAC	CTTCAACCTGGAGGGTGT CAGCCCGACGACTAGTGAC	2322
Db	2053	ACGAGGGGTACTTGCAC	CTTCAACCTGGAGGGTGT CAGCCCGACGACTAGTGAC	2112
Qy	2323	CTGCGCTTGCAGCTGTGG	GTGTGGAGTGGGAGCGGAGAGCTTTCAGCATCAAC	2382
Db	2113	CTGCGCTTGCAGCTGTGG	GTGTGGAGTGGGAGCGGAGAGCTTTCAGCATCAAC	2172
Qy	2383	TTCAACATCAACAGGACA	CAAGGCTTTGCTGTGCTCTGTGGAGAGTGAAGCGGG	2442

Db 2173 TTCAACATACCAAGGACACAGGTTTGCTAGCTGCTGGCTCTGGAGAGTGAAGCGGG 2232
Qy 2443 GTCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCTTCCCTCATTTCCGCGAGAATATA 2502
Db 2233 GTCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCTTCCCTCATTTCCGCGAGAATATA 2292
Qy 2503 ATTTCAGCCCTGAGCCACCCCTGTAGCGGGGTGCCAGTGGCGGACTCTGGCCCGAGAAA 2562
Db 2293 ATTTCAGCCCTGAGCCACCCCTGTAGCGGGGTGCCAGTGGCGGACTCTGGCCCGAGAAA 2352
Qy 2563 CTCACCTGGACGCCATCTCAGCTTCTTTGGCTTCCAAAGCCAGCCGCCACAGCCATGATC 2622
Db 2353 CTCACCTGGACGCCATCTCAGCTTCTTTGGCTTCCAAAGCCAGCCGCCACAGCCATGATC 2412
Qy 2623 CTCACCTGTGGAGGCGCGCACTTCCCAAGCGCAACCTCAGCCAGCTGGCTGCAGCA 2682
Db 2413 CTCACCTGTGGAGGCGCGCACTTCCCAAGCGCAACCTCAGCCAGCTGGCTGCAGCA 2472
Qy 2683 GTGGCTGGACTGGCCAGCCAGAGCGCTGGCTCTTTCACAGTGTCCGAGGCTGAGTGTGA 2742
Db 2473 GTGGCTGGACTGGCCAGCCAGAGCGCTGGCTCTTTCACAGTGTCCGAGGCTGAGTGTGA 2532
Qy 2743 GGCGGCCAG 2752
Db 2533 GGCGGCCAG 2542

RESULT 5

US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: PS026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR FILING DATE: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR FILING DATE: 2002-08-19
; PRIOR FILING DATE: 2002-08-19
; PRIOR FILING DATE: 2002-08-21
; PRIOR FILING DATE: 2002-08-21
; PRIOR FILING DATE: 2002-09-23
; PRIOR FILING DATE: 2002-09-23
; PRIOR FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-948-518-77

Query Match 85.68; Score 2356; DB 21; Length 3561;
Best local Similarity 93.68; Pred. No. 0;
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;
Qy 43 GCCATGGCCGCTCGCGGCCGCGCTGTGGCCAGCGCTCTCTGGGCATAGTCTCTCGCGGCTGG 102

Db 1 GCCATGGCCGCTCGCGGCCGCGCTGTGGCCAGCGCTCTCTGGGCATAGTCTCTCGCGGCTGG 60
Qy 103 CTCGCGGGCTCGGGTCCAGCAGAGTGCACCGTGGCCAAACCCAGTGCCTGTGTGCCAAC 162
Db 61 CTCGCGGGCTCGGGTCCAGCAGAGTGCACCGTGGCCAAACCCAGTGCCTGTGTGCCAAC 120
Qy 163 CCGGACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGATGTGTACATCTGTCAAGAACAG 222
Db 121 CCGGACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGATGTGTACATCTGTCAAGAACAG 180
Qy 223 CAGTGTCTGTCTGTGGAGGCGCTGCGGCCACCGCAGATCTTCTCAAGTGCACCGG 282
Db 181 CAGTGTCTGTCTGTGGAGGCGCTGCGGCCACCGCAGATCTTCTCAAGTGCACCGG 240
Qy 283 GAGTGGTGGCCAGGTGGACACGTCAGCGCAGCACAGACGGGAGCAGTGGGCTG 342
Db 241 GAGTGGTGGCCAGGTGGACACGTCAGCGCAGCACAGACGGGAGCAGTGGGCTG 300
Qy 343 CCACCATGGAGTCCGCAATTAATGTCTAAGCGCAGAGTTCAGAAAGTGTTCGGGCTG 402
Db 301 CCACCATGGAGTCCGCAATTAATGTCTAAGCGCAGAGTTCAGAAAGTGTTCGGGCTG 360
Qy 403 GAGGAATACTGGTCCAGTGCAGTGCATGAGTCTCTCGGGCACACCAAGAGTCAAGAG 462
Db 361 GAGGAATACTGGTCCAGTGCAGTGCATGAGTCTCTCGGGCACACCAAGAGTCAAGAG 420
Qy 463 GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCAGCAGGAGCGCTGGCCAGGAG 522
Db 421 GCCTACATCCGCATAGCCATATTTTGGCAAGAACTTCAGCAGGAGCGCTGGCCAGGAG 480
Qy 523 GTGTCTCTGGAGCAGGCGATCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
Db 481 GTGTCTCTGGAGCAGGCGATCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 583 GAGTGGAGTGGTCCCGAACGAGGACCTGGTGGACCGCTCCCTGGAACCCCAATGTATAC 642
Db 541 GAGTGGAGTGGTCCCGAACGAGGACCTGGTGGACCGCTCCCTGGAACCCCAATGTATAC 600
Qy 643 ATCAGCGGAGCAGACCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 702
Db 601 ATCAGCGGAGCAGACCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660
Qy 703 ACCTGGTGGCCAAAGACATCGTGGCAGCTGCGCGCAGCGCTCCGCTGTGTCTCATCGTC 762
Db 661 ACCTGGTGGCCAAAGACATCGTGGCAGCTGCGCGCAGCGCTCCGCTGTGTCTCATCGTC 720
Qy 763 TACGTGAACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 822
Db 721 TACGTG----- 726
Qy 823 CGCGGCTGGCAGAAACGGAGCCGAGTGCACCAACCGCGGCGCTCTCTCAACGGGGGCGCT 882
Db 727 ----- 726
Qy 883 TTCTGTGAGGGGCGAGAATGTCCAGAAAAACAGCCTGGCCACCCCTGTGCCCATAGACGC 942
Db 727 -----GACGGC 732
Qy 943 AGCTGGAGCCCGTGGAGCAAGTGGTGGGCTGTGGGCTGGAGTGCACCCACTGCGCGAGC 1002
Db 733 AGCTGGAGCCCGTGGAGCAAGTGGTGGGCTGTGGGCTGGAGTGCACCCACTGCGCGAGC 792
Qy 1003 CGTGAAGTGTCTGACCCAGCACCCCGCAACGGAGGGAGAGTGCACGGGACATGACCTG 1062
Db 793 CGTGAAGTGTCTGACCCAGCACCCCGCAACGGAGGGAGAGTGCACGGGACATGACCTG 852
Qy 1063 GACACCGCAACTGTACCAAGTGCCTGTGTGTACAGTGTCTTCTGCGCCCTGAGGAGCTG 1122
Db 853 GACACCGCAACTGTACCAAGTGCCTGTGTGTGTACACTGTGTGTGTGTGTGTGTGTGTGT 912
Qy 1123 GCCTCTATGTGGGCTCATCGCGGCTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1182

; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: misc_feature									
; OTHER INFORMATION: Incyte ID No. US2004002324A1 6052371CB1									
US-10-311-623-13									
Query Match 85.6%; Score 2356; DB 17; Length 3580;									
Best Local Similarity 93.6%; Pred. No. 0;									
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;									
Qy	43	GCCATGCGCTGCCGCGCCGCGCTGTGGCCAGCGCTCTGGGCATAGTCTCGCGCTTGG	102						
Db	1	GCCATGCGCTGCCGCGCCGCGCTGTGGCCAGCGCTCTGGGCATAGTCTCGCGCTTGG	60						
Qy	103	CTCGCGGCTGGGTGCCAGCAGAGTGCCACCGTGGCCAAACCCAGTCTGTGGCCAAAC	162						
Db	61	CTCGCGGCTGGGTGCCAGCAGAGTGCCACCGTGGCCAAACCCAGTCTGTGGCCAAAC	120						
Qy	163	CCGGACCTGCTCCCACTTCTTGGTGGAGCCGAGATGTGTACATCGTCAAGAACAG	222						
Db	121	CCGGACCTGCTCCCACTTCTTGGTGGAGCCGAGATGTGTACATCGTCAAGAACAG	180						
Qy	223	CCAGTGTCTGTGTGCAAGGCGCTGCCGCCACGACAGATCTTCTCAAGTGCAACGGG	282						
Db	181	CCAGTGTCTGTGTGCAAGGCGCTGCCGCCACGACAGATCTTCTCAAGTGCAACGGG	240						
Qy	283	GAGTGGTGGCCAGGTGGACCAAGTATCGAGCGCAGCAGACGCGGAGTGTGGGCTG	342						
Db	241	GAGTGGTGGCCAGGTGGACCAAGTATCGAGCGCAGCAGACGCGGAGTGTGGGCTG	300						
Qy	343	CCACCAATGAGGTCCGCATTAATGTCTCAAGCAGAGTCTCGAGAGTGTTCGGGCTG	402						
Db	301	CCACCAATGAGGTCCGCATTAATGTCTCAAGGAGCAGGTCTCGAGAGTGTTCGGGCTG	360						
Qy	403	GAGGAATACTGGTCCAGTGGGCACTGGAGTCTCTCGGGCACCAACAGAGTCAAGAG	462						
Db	361	GAGGAATACTGGTCCAGTGGGCACTGGAGTCTCTCGGGCACCAACAGAGTCAAGAG	420						
Qy	463	GCCTACATCCGCATPAGCCAGTATGCGCAAGAACTTCGAGCAGAGCGCTGGCCAAAGAG	522						
Db	421	GCCTACATCCGCATPAGCCAGTATGCGCAAGAACTTCGAGCAGAGCGCTGGCCAAAGAG	480						
Qy	523	GTGTCCCTGGAGCAGGCGATCGTGTCCCTCGCGTCCACCGGAGGCGATCCCTCCAGCC	582						
Db	481	GTGTCCCTGGAGCAGGCGATCGTGTCCCTCGCGTCCACCGGAGGCGATCCCTCCAGCC	540						
Qy	583	GAGTGGAGTGGTTCGGAAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATAC	642						
Db	541	GAGTGGAGTGGTTCGGAAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATAC	600						
Qy	643	ATCAACGGGAGCAGACGCTGGTGGCGACAGGCCCGCTTGTGTGACACGGCCAACTAC	702						
Db	601	ATCAACGGGAGCAGACGCTGGTGGCGACAGGCCCGCTTGTGTGACACGGCCAACTAC	660						
Qy	703	ACCTGCGTGGCCAGAACATCGTGGCAGTGGCGCAGCGCTCCGCTGTGTCTATGCTC	762						
Db	661	ACCTGCGTGGCCAGAACATCGTGGCAGTGGCGCAGCGCTCCGCTGTGTCTATGCTC	720						
Qy	763	TACGTGAACGCTGGGTGGTGGACGCTGGACCGAGTGGTCCGCTCTGCGACGCGAGTGGG	822						
Db	721	TACGTG-----	726						
Qy	823	CGCGGCTGGCAGAAACGGAGCCGAGGTGCACCAACCCCGCGGCTCTCAACGGGGGGGCT	882						
Db	727	-----	726						
Qy	883	TTCTGTGAGGGGAGATGTCCAGAAAACAGCTGGCCACCTGTGTGCCCAAGTAGACGGC	942						
Db	727	-----GACGGC	732						
Qy	943	AGCTGGAGCCGTGGAGCAAGTGTGCGGCTGTGGGCTGTGAGCTGTGACACCCACTGCGGAGC	1002						
Db	733	AGCTGGAGCCGTGGAGCAAGTGTGCGGCTGTGGGCTGTGAGCTGTGACACCCACTGCGGAGC	792						

Qy	1003	CGTGAGTGTCTTGACCCAGCACCCCGCAACGGAGGGAGAGTGCACAGGCACTGACCTG	1062						
Db	793	CGTGAGTGTCTTGACCCAGCACCCCGCAACGGAGGGAGAGTGCACAGGCACTGACCTG	852						
Qy	1063	GACACCGGCAACTGTACCACTGTGTGTACACAGTGTCTTGGCCCTGAGGAGCTG	1122						
Db	853	GACACCGGCAACTGTACCACTGTGTGTACACAGTGTCTTGGCCCTGAGGAGCTG	912						
Qy	1123	GCCTCTATGTGGGCTCATCGCGCTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTC	1182						
Db	913	GCCTCTATGTGGGCTCATCGCGCTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTC	972						
Qy	1183	ATCCTCGTTTATTTGCGGAGAAAGAGGGGCTGGAATCAGATGTGGTGAATCGTTCATT	1242						
Db	973	ATCCTCGTTTATTTGCGGAGAAAGAGGGGCTGGAATCAGATGTGGTGAATCGTTCATT	1302						
Qy	1243	CTCACCTCAGGCTTCCAGCCCGTCAAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	1302						
Db	1033	CTCACCTCAGGCTTCCAGCCCGTCAAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	1092						
Qy	1303	CTCACCATCCAGCGGACCTCAGCACCAACCAACCACTTACAGGGGAGTCTCTGTGCC	1362						
Db	1093	CTCACCATCCAGCGGACCTCAGCACCAACCAACCACTTACAGGGGAGTCTCTGTGCC	1152						
Qy	1363	CGGAGGATGGGCGCCAGCCCAAGTTCAGCTCAACATGGGCACTGTCTCAGCCGCTG	1422						
Db	1153	CGGAGGATGGGCGCCAGCCCAAGTTCAGCTCAACATGGGCACTGTCTCAGCCGCTG	1212						
Qy	1423	GGTGGGCGCGCCACACACTGACACCACTCTCCACCTCTCAGGCGGAGGATTCGTC	1482						
Db	1213	GGTGGGCGCGCCACACACTGACACCACTCTCCACCTCTCAGGCGGAGGATTCGTC	1272						
Qy	1483	TCCGCGCTCTCCACCCAGAACTACTTCCGCTCCCTCCCGAGGCGCACAGCAACATGACC	1542						
Db	1273	TCCGCGCTCTCCACCCAGAACTACTTCCGCTCCCTCCCGAGGCGCACAGCAACATGACC	1332						
Qy	1543	TATGGGACCTTCAACTTCTCGGGGCGCGCTGATATCCCTAATACAGTATCAGGCTC	1602						
Db	1333	TATGGGACCTTCAACTTCTCGGGGCGCGCTGATATCCCTAATACAGGAAATCAGGCTC	1392						
Qy	1603	CTCATCCCCCAGATGCCATACCCCGAGGAGATCTATGAGATCTACCTCAGCTGCAC	1662						
Db	1393	CTCATCCCCCAGATGCCATACCCCGAGGAGATCTATGAGATCTACCTCAGCTGCAC	1452						
Qy	1663	AAAGCCGGAAGACGTGAGTGTGCCCTAGCTGGCTGTGAGACCTCTGAGTCCCATCGTT	1722						
Db	1453	AAAGCCGGAAGACGTGAGTGTGCCCTAGCTGGCTGTGAGACCTCTGAGTCCCATCGTT	1512						
Qy	1723	AGCTGTGGACCCCTGGGCTCTGCTCAACCGGCGAGTCACTCTGGCTATGGACCACTGT	1782						
Db	1513	AGCTGTGGACCCCTGGGCTCTGCTCAACCGGCGAGTCACTCTGGCTATGGACCACTGT	1572						
Qy	1783	GGGAGCGCCAGCCCTGACAGCTGAGCTGCGCTCAAAAAGCAGTCTGCGAGGGGAGC	1842						
Db	1573	GGGAGCGCCAGCCCTGACAGCTGAGCTGCGCTCAAAAAGCAGTCTGCGAGGGGAGC	1632						
Qy	1843	TGGGAGGATGTGTGCACTTGGGCGGAGGCGCCCTCCCACTCTACTCTGCGAGCTG	1902						
Db	1633	TGGGAGGATGTGTGCACTTGGGCGGAGGAGGCGCCCTCCCACTCTACTCTGCGAGCTG	1692						
Qy	1903	GAGGCGAGTGTGCTTACGCTTTCAGGAGCAGCTGGGCGGCTTGGCCCTGTTGGGAGAG	1962						
Db	1693	GAGGCGAGTGTGCTTACGCTTTCAGGAGCAGCTGGGCGGCTTGGCCCTGTTGGGAGAG	1752						
Qy	1963	GCCTCAGGCTGCTGCGCGCAAGCGCTCAAGCTGCTTCTGCTTGGCGCGGTGGCTGC	2022						
Db	1753	GCCTCAGGCTGCTGCGCGCAAGCGCTCAAGCTGCTTCTGCTTGGCGCGGTGGCTGC	1812						
Qy	2023	ACCTCCCTCGAGTACAACTCCGGGCTACTGTGCTGCAAGACCAACCAACGATGCACTCAAG	2082						
Db	1813	ACCTCCCTCGAGTACAACTCCGGGCTACTGTGCTGCAAGACCAACCAACGATGCACTCAAG	1872						

Qy 2083 GAGGTGGTGCAGCTGGAGAGCAGCTGGGGGACAGCTGATCCAGAGCCACGGGTCTGT 2142
Db 1873 GAGGTGGTGCAGCTGGAGAGCAGCTGGGGGACAGCTGATCCAGAGCCACGGGTCTGT 1932
Qy 2143 CACTTCAAGGACAGTTACCAAACTGGGGCTATCCATCCAGATGGCCAGCTCCCTG 2202
Db 1933 CACTTCAAGGACAGTTACCAAACTGGGGCTATCCATCCAGATGGCCAGCTCCCTG 1992
Qy 2203 TGAAGAGTAAAGTCTCTGTGTCAGCTACCAAGAGATCCCTTTTATCATCATCTGGAATGGC 2262
Db 1993 TGAAGAGTAAAGTCTCTGTGTCAGCTACCAAGAGATCCCTTTTATCATCATCTGGAATGGC 2052
Qy 2263 ACGCAGGGTACTTGCACCTTCACTCCCTGAGCGGTGTGAGCCCGCAGCACTAGTGAC 2322
Db 2053 ACGCAGGGTACTTGCACCTTCACTCCCTGAGCGGTGTGAGCCCGCAGCACTAGTGAC 2112
Qy 2323 CTGGCTGCAAGCTGTGGGTGTGAGGTGTGAGGGGCGAGCGGCGAGGTTTCAAGTCAAC 2382
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Qy 2383 TTCAACATCACCAAGGACCAAGGTTTGTGAGCTGTGCTGTGGAGGTGAAGCGGG 2442
Db 2173 TTCAACATCACCAAGGACCAAGGTTTGTGAGCTGTGCTGTGGAGGTGAAGCGGG 2232
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Qy 2503 ATTTCCAGCTGGACCCACCTGTAGGGGGGTGCGACTGGCGGACTCTGGCCCGAGAA 2562
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Qy 2563 CTCCACCTGGACAGCATCTCAGCTTCTTTGGCTCCAAAGCCCGCCAGCCCGCATGTC 2622
Db 2353 CTCCACCTGGACAGCATCTCAGCTTCTTTGGCTCCAAAGCCCGCCAGCCCGCATGTC 2412
Qy 2623 CTCAACCTGTGGGAGGCGCGCACTTCCCAAGCGCAACCTCAGCCAGCTGGCTGCAGCA 2682
Db 2413 CTCAACCTGTGGGAGGCGCGCACTTCCCAAGCGCAACCTCAGCCAGCTGGCTGCAGCA 2472
Qy 2683 GTGGCTGGACTGGGCGGCGAGCGCTGGCTTCTTCAAGTGTGGAGGCTGAGTGTGA 2742
Db 2473 GTGGCTGGACTGGGCGGCGAGCGCTGGCTTCTTCAAGTGTGGAGGCTGAGTGTGA 2532
Qy 2743 GGCGGGCCAG 2752
Db 2533 GGCGGGCCAG 2542

RESULT 7

US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US2003004046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, B. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1

Query Match 82.1%; Score 2259; DB 10; Length 3014;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 2427; Conservative 0; Mismatches 280; Indels 0; Gaps 0;
Qy 46 ATGGCGCTCCGGCCCGGCTGTGGCCAGCGCTCTGGGCATAGTCCTCGCGCTTGGCTC 105
Db 1 ATGGCGCTCCGGCCCGGCTGTGGCCAGTGTCTCTGGGCATAGTCCTCGCGCTTGGCTT 60
Qy 106 CGGGGCTCGGGTCCCGCAGAGTGCCACCGTGGCCAGCCAGTGGCTGGTCCCAACCCG 165
Db 61 CGTGGTTCGGGTGCCAGCAGAGTGCCACCGTGGCCAAATCCAGTGGCCGTTGCCAAGCCC 120
Qy 166 GACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGAGTGTGTACATCGTCAAGAAACAAGCCA 225
Db 121 GACCTGCTGCCCCACTTCTCTGGTAGAGCTTGAGGACGTGTACATTGTCAAGAACAGCCG 180
Qy 226 GTGCTGCTGTGTGCAAGGCGCTGCCCGCCACCGACATCTTCTTCAAGTGCACCGGGAG 285
Db 181 GTGTTGTGTGTGCAAGGCTGTGCTCCGCCACCGACATCTTCTTCAAGTGCACATGGGGA 240
Qy 286 TGGGTGGCCAGGTGGACACAGCTGTGAGCGGAGCAGACAGCGGAGCAGTGGGCTGCC 345
Db 241 TGGGTGGCCAGGTGCGATCACGTAATGAAACGAGCAGCAGCGGAGTGGCA 300
Qy 346 ACCATGGAGTCCGCATTAAATGTCTCAAGGACAGGTGCGAGAGGTGTTCCGGCTGGAG 405
Db 301 ACCATGGAGTCCGATCAACGTATCGAGGACAGAGGTAGAGAAAGTGTGTTGGCTGGAG 360
Qy 406 GAATACGTGGTCCAGTGGGTGGCATGGAGTCTCTGGGGCACACCAAGAGTCAAGAGGCC 465
Db 361 GAATACGTGGTCCAGTGGGTGGCATGGAGTCTCTGGGGTACCAACCAAGTCAAGAGGCC 420
Qy 466 TACATCCGATAGCCAGATTGCCAAGAACTTCCAGCAGAGCGCTGGCCAGGAGGTG 525
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Qy 526 TCCCTGGAGCAGGGCATCGTGTGCTGCTGCGCTCCACCGGAGGGCATCCCTCCAGCCGAG 585
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Db 601 ACGCGGAGCAGACCTGTGGTGGCAGAGGGCCGCTTGTCTGAGCCGACACGCGCAATACACC 660
Qy 706 TGGGTGGCCAAAGAAACATCGTGGCAGCGTGGCGGAGCGGCTCCGCTGCTGTCTATC 765

Leonardo, E. David
 Hink, Lindsay
 Masu, Masayuki
 Kazuko, Keino-Masu
 TITLE OF INVENTION: Netrin Receptors
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/256,702
 FILING DATE: 27-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/933,261
 FILING DATE: 20-Aug-2001
 APPLICATION NUMBER: 08/808,982
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: UC96-217
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3014 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 us-10-256-702-1

Query Match 82.1%; Score 2259; DB 14; Length 3014;
 Best Local Similarity 89.7%; Pred. No. 0;
 Matches 2427; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

46 ATGGCCGTCGCGCCGCGCTGTGGCCAGCGCTCTGGGCATAGTCTCTGGCGCTGGCTC 105
 1 ATGGCCGTCGCGCCGCGCTGTGGCCAGTGTCTCTGGGCATAGTCTCTGGCGCTGGCTT 60
 106 CGCGGCTCGGGTCCGACAGAGTGCCACCGTGGCCAAACCGAGTGGCTGGCCAAACCG 165
 61 CGTGGTTCGGGTGCGCCAGCAGAGTGCCACGCTGGCCAAATCCAGTGGCCGCTGGCCAAACCG 120
 166 GACCTGCTTCCCACTTCTCTGGTGGAGCGTGTACATGTCGTCAGAAACAGCCCA 225
 121 GACCTGCTGCCCCACTTCTCTGGTGGAGCGTGGAGCGTGTACATGTCAGAAACAGCCG 180
 226 GTGCTGCTGTGTGCAAGGCGGTGCGCCGACGAGATCTTCTTCAAGTGCACAGGGAG 285
 181 GTGTTGTGTGTCAGAGGCTGTGCTGCGCCACCGAGATCTTCTTCAAGTGCATGGGGAA 240
 286 TGGTGGCCGAGGTGGACAGGTGATCGAGCGCAGCAAGAGGAGGAGTGGCTGCCC 345
 241 TGGGTTCGCGCAGGTGCGATCAGTAAATTGAAACGACGACCCGACAGCAGCAGCGGATGGCCA 300
 346 ACCATGGAGGTCCGCAATTAATGCTCAAGGCGAGCAGGTTCGAGAGGTTTCGGGCTGGAG 405
 301 ACCATGGAGGTCCGCAATTAACGATTCAGGCGAGCAGGTAGAGAAAGTTTGGGCTGGAG 360
 406 GAATACCTGTCAGTGTGGCATGGAGTCTCTCGGGGCACCAAGAGAGTCAAGAGGCC 465

Db 361 GAATACCTGTCAGTGTGGCATGGAGTCTCTCGGGTACCAACAAAGTCAAGAGGCC 420
 Qy 466 TACATCCGCATAGCCAGATTGGCGAAGAACTTCAGCAGAGGCGCTGGCCAAAGAGGTG 525
 Db 421 TACATCCGCATTGCTTATTTGGCGAAGAACTTTAGCAGAGGACCCACTGGCCAAAGAGGTG 480
 Qy 526 TCCCTGAGCAGGAGCATCGTCTGCGCTGCGCTCCACCGAGGAGGATCCCTCCAGCCGAG 585
 Db 481 TCACTGGAGCAAGGCATTGTACTTGTGCGCCCCCAGAGAGGAATCCCCCCAGCTGAG 540
 Qy 586 GTGAGTGGCTTCGGAACAGAGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATATATC 645
 Db 541 GTGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTATATC 600
 Qy 646 ACGCGGAGCAGACCGCTGGTGGCAGAGCGCGCTTCTGTGACAGCGCAACTATACACC 705
 Db 601 ACGCGGAGCAGACCGCTTAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660
 Qy 706 TGGCTGGCCAAAGAACATCGTGGCAGCGCTGGCGAGCGCTCCGCTGTGTCTATCTCTAC 765
 Db 661 TGTGTGGCCAAAGAACATCGTAGCCGTCGCGAAGCACCTCTGCAGCGGTCAATTTAT 720
 Qy 766 GTGAACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 825
 Db 721 GTGAACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
 Qy 826 GGCCTGGCAGAAACGGAGCGGAGTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTC 885
 Db 781 GGCCTGGCAGAAACGGAGCGGAGTGCACCAACCGCGCGCTCTCTCAACGGGGCGCTTTC 840
 Qy 886 TGTGAGGGGCGAGAAATGTCCAGAAAAACAGCTGGCGCCACCTGTGCCAGTAGACGGAGC 945
 Db 841 TGTGAGGGGCGAGAAATGTCCAGAAAAACAGCTGGCGCCACTCTGTGCCAGTAGACGGAGC 900
 Qy 946 TGGAGCCCGTGGAGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1005
 Db 901 TGGAGTTCGTGGAGTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
 Qy 1006 GAGTGTCTGACCCAGCACCCCGCAGAGGGGAGAGTGGCCAGGCGACCTGACCTGGAC 1065
 Db 961 GAGTGTCTGACCCAGCACCCCGCAGAGGGTGGAGAGTGGGGGTGTGCGGGTGTGACCTGGAC 1020
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 Db 1021 ACCCGCAACTGTACAGTGACCTCTGTGTGCAACACCGCTTCTTGGCCCGAGGAGCTGGCT 1080
 Qy 1126 CTCTATGTGGGCTCTATCGCGCTGGCGCTGTGCTGGTCTGTGCTGTGCTGTGCTGTGCT 1185
 Db 1081 CTCTATGTGGGCTCTATCGCGCTGGCGCTGTGCTGGTCTTCTTGTGCTGTGCTGTGCTGGA 1140
 Qy 1186 CTGTTTATTTCCGGAAGAGGAGGGCTGGACTCAGATGTGGTGTGCTGTGCTGTGCTGTGCT 1245
 Db 1141 CTCAATTTACTGTGCGAAGAGGAGGGCTGGATCCGATGTGGCGAGCTGTGCTCATCTTC 1200
 Qy 1246 ACCTCAGGCTTCCAGCCCGCTCAGCATCAAGCCAGCAAGAGAGAGAGAGAGAGAGAGAG 1305
 Db 1201 ACCTCAGGCTTCCAGGCTGTGAGCATCAGCCAGCAAGAGAGAGAGAGAGAGAGAGAG 1260
 Qy 1306 ACCATCCAGCCGAGCTCAGCAACCAACCAACCACTTACAGGAGAGTCTGTGTCCCGG 1365
 Db 1261 ACCATCCAGCCGAGCTCAGCAACCAACCACTTACAGGAGAGTCTGTGTCCAGG 1320
 Qy 1366 CAGATGGGGCCAGCGCCCAAGTTCAGTCAACCAATGGGACCTGTGTGAGGAGAGAGAGAG 1425
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 Qy 1426 GCGGGCGCCAGCAGCTGTGACAGCTCTCCACCTCTCAGGCGCAGGAGAGTGTGCTCTCC 1485
 Db 1381 AGTGGCGCCAGTGTGACAGCTTACCACTTACCACTTCTGTGAGGCTGTGAGGAGTGTGCTCTCC 1440
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Db 1441 CGCTCTCCACCCAAAATACTTTTCGTTCCCTGCCCGCGCACCAACATGGCCCTAC 1500
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Db 1501 GGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC 1560
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Db 1561 ATACCCCGGATGCCATCCCGCGAGGAAGATCTACAGATCTACCTCACACTGCACAAG 1620
Qy 1666 CCGGAAGACGTGAGTTGGCCCTAGCTGGCTGTGAGACCTGTGAGTCCCATCTGTTAGC 1725
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Qy 1726 TGTGGAACCCCTGGCGTCTGCTCACCCGCGCAAGTCACTCTGGCTATGGAACCACTGTTGG 1785
Db 1681 TGTGGGCCCCAGAGTCTGCTCACCCGCGCAAGTCACTCTGGCTATGGAACCACTGTTGG 1740
Qy 1786 GAGCCACGCTGACAGCTGGAGCTGGGCTCAAAAGCAGTCTGTGGAGGGGAGCTGG 1845
Db 1741 GAGCCACGCTGACAGCTGGAGCTGGGCTCAAAAGCAGTCTGTGGAGGGGAGCTGG 1800
Qy 1846 GAGGATGTGCTGACCTGGGCGAGGAGCGCCCTCCCACTCTACTACTGCCAGCTGGAG 1905
Db 1801 GAGGATGTGCTGACCTGGGCGAGGAGCTGGGCTCAAAAGCAGTCTGTGGAGGGGAG 1860
Qy 1906 GCCAGTGCCTGCTACGTCTTCAACGAGCAGCTGGGCGCTTGTGCTGTGGAGAGGCC 1965
Db 1861 GCCGGGCGCTGCTATGTCTTCAACGAGCAGCTGGGCGCTTGTGCTGTGGAGAGGCC 1920
Qy 1966 CTCAGCTGGCTGCGCGCAAGCGCTCAAGTGTCTGTTTGGCGGCTGGCTGCACC 2025
Db 1921 CTCAGCTGGCTGCGCGCAAGCGCTCAAGTGTCTGTTTGGCGGCTGGCTGCACC 1980
Qy 2026 TCCCTCGAGTACAACATCCGGGTCTACTGCTGCTGACACCAACAGATGCACTCAAGGAG 2085
Db 1981 TCCCTCGAGTACAACATCCGGGTCTACTGCTGCTGACACCAACAGATGCACTCAAGGAG 2040
Qy 2086 GTGTGTGAGTGGAGAAAGCTGGGGGAGCAGCTGATCAGGAGCCACGGGTCTGTGCAC 2145
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Qy 2146 TTCAAGACAGTGTACACACCTGCGCTATCCATCCACGATGTCAGCTGCTGCTGG 2205
Db 2101 TTCAAGACAGTGTACACACCTGCGCTATCCATCCACGATGTCAGCTGCTGCTGG 2160
Qy 2206 AAGAGTAAAGTCTCTGTGACGTACAGGAGATCCCTTTTATCACATCTGGAATGGCAG 2265
Db 2161 AAGAGTAAAGTCTCTGTGACGTACAGGAGATCCCTTTTATCACATCTGGAATGGCAG 2220
Qy 2266 CAGCGGTACTTGTGACCTGCACTTCACTGAGGAGTGTAGCCCCAGCATAGTGAACCTG 2325
Db 2221 CAGCAGTATCTGCACTGCACTTCACTGAGGAGTGTAGCCCCAGCATAGTGAACCTG 2280
Qy 2326 GCCTGCAAGCTGTGGGTGTGCGAGGTGAGGGGAGCGGCGAGAGCTTTCAGCATCACTTC 2385
Db 2281 GCCTGCAAGCTGTGGGTGTGCGAGGTGAGGGGAGCGGCGAGAGCTTTCAGCATCACTTC 2340
Qy 2386 AACATCAACAGGACACAAAGTTTGTGCTGAGCTGTGCTGCTGAGAGTGAAGGGGGGTC 2445
Db 2341 AACATCAACAGGACACAAAGTTTGTGCTGAGAGTGAAGGGGGGTC 2400
Qy 2446 CCAGCCCTGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTTGGGCGAAGATTAATT 2505
Db 2401 CCAGCCCTGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTTGGGCGAAGATTAATT 2460
Qy 2506 TCAGAGCTGGACCCACCTGTAGCGGGGTGCGACCTGGCGGACTCTGGCCGAGAACTC 2565
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Qy 2566 CACCTGACAGCCATCTCAGCTCTTTTGGCTTCAAGGCCAGCCCCACAGCCATGATCCTC 2625
Db 2521 CACCTGACAGCCATCTCAGCTCTTTTGGCTTCAAGGCCAGCCCCACAGCCATGATCCTC 2580

RESULT 9

US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15

Query Match 81.8%; Score 2252.2; DB 16; Length 2697;

Best Local Similarity 89.7%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

Qy 46 ATGCGCGTCCGGCGCGCGCTGTGCGCAGAGCTCTCTGGGCATAGTCTCTCGCGCTTGGCTC 105
Db 1 ATGCGCGTCCGGCGCGCGCTGTGCGCAGAGCTCTCTGGGCATAGTCTCTCGCGCTTGGCTC 60
Qy 106 CGCGGCTCGGGTCCCGCAGCAGAGTGCACCGTGGCCAAACCCAGTGTGTGCAACCCG 165
Db 61 CGTGTTCGGGTGCCCGCAGCAGAGTGCACCGTGGCCAAATCCAGTGCCTGCGGTCACACCC 120
Qy 166 GACCTGTTCCCACTTCTGTTGGAGCCCGAGAGTGTGTACATCGTCAAGAACAGCCA 225
Db 121 GACCTGTTCCCACTTCTGTTGGAGCCCGAGAGTGTGTACATCGTCAAGAACAGCCA 180
Qy 226 GTGCTGTTGTGTGAAGCGCGTGGCCGACAGATCTTCTCAAGTGCACCGGGAG 285
Db 181 GTGTTGTTGTGTGAAGCGTGTGCTGCGACCCAGATCTTCTCAAGTGCACCGGGAG 240
Qy 286 TGGGTGCGCCAGTGGACCAACGTGATCGAGCGCAGCAGACCGGAGCAGTGGGCTGCC 345
Db 241 TGGGTGCGCCAGTGGACCAACGTGATCGAGCGCAGCAGACCGGAGCAGTGGGCTGCC 300
Qy 346 ACCATGAGGTTCGCGATTATGTCTCAAGCAGCAGGTTCGAGAGGTTCGGGCTGGAG 405
Db 301 ACCATGAGGTTCGCGATTATGTCTCAAGCAGCAGGTTCGAGAGGTTCGGGCTGGAG 360
Qy 406 GAATACTGGTCCAGTGGCGTGGCATGGAGTCTCTCGGGCACCAACAGAGTCAAGAGGCC 465
Db 361 GAATACTGGTCCAGTGGCGTGGCATGGAGTCTCTCGGGTACCAACAGAGTCAAGAGGCC 420
Qy 466 TACATCCGATAGCCAGATTCGCAAGAACTTTCAGCAGAGCGCTGTGGCCAGAGGAGTG 525
Db 421 TACATCCGATAGCCAGATTCGCAAGAACTTTCAGCAGAGCGCTGTGGCCAGAGGAGTG 480

Qy 526 TCCCTGGAGCAGGCGATCGTCTGCCCTGCCGTCCACCGAGGGGCATCCCTCCAGCCGAG 585
Db 481 TCATCGAGCAAGCAATTGTACTACCTTGTGCCCCCAGAGGATCCCTCCAGCTGAG 540
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Db 601 ACGGGGAGCAGACCTAGTGGTCCGCTCAGGCCCGCTTGGCCGACAGGCCCAACTACACC 660
Qy 706 TGCCTGGCCAAAGAAATCATGTGGACGCTGGCCGACGCGCTCCGCTGCTGTATCATGCTTAC 765
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Qy 1186 CTGTTTTATTGGCGGAAGAGGGGCTGGACTCAGATGTGGCTGTGCTGTGCTGTGCTGTGCTC 1245
Db 1141 CTCTATTTACTGTGCAAGAGGAGGGCTGGACTCCGATGTGGCGACTCTGTCTCATCTTC 1200
Qy 1246 ACCTCAGGCTTCCAGCCCGTCAAGCATCAAGCCCAAGCAAGCAGCAACCCCACTGTGCTC 1305
Db 1201 ACCTCGGGCTTCCAGCCCTGTCAAGCATCAAGCCCAAGCAAGCAGCAACCCCACTGTGCTC 1260
Qy 1306 ACCATCAGCGGACCTCAGGACACCAACCACTTACAGGGGAGTCTGTGCCCCGG 1365
Db 1261 ACCATCAGCGGACCTCAGGACACCACTTACAGGGGAGTCTGTATGTTCGAGG 1320
Qy 1366 CAGGATGGGCGGACCCCAAGTTCAGCTCAACCAATGGGCACTGTGCTCAGCCCGCTGGGT 1425
Db 1321 CAGGATGGACCCAGCCCAAGTTCAGCTCTAATGGTCACTGTGCTCAGCCCACTGGGG 1380
Qy 1426 GGGGGCGGCAACACATGTGACACAGCTCTCCCACTCTGAGGCGGAGGATTCGTCTCC 1485
Db 1381 AGTGGCGGCCATACGTTTGCACCAAGCTCACCACCTCTGAGGCTGAGGACTTCGTCTCC 1440
Qy 1486 GGCCTCTCCACCCAGAAATCTATTCGCTCCGCTCCGCGGACACAGCAACATGACCTAT 1545
Db 1441 GGCCTCTCCACCCAAATCTATTTCTGTTTCCGCTCCGCGGACACAGCAACATGGCCCTAC 1500
Qy 1546 GGGACCTTCACTTCTCCGGGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1605
Db 1501 GGGACCTTCACTTCTCCGGGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Qy 1606 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAAGCTGCAAG 1665

Db 1561 ATACCCCGGATGCCATCCCGGAGGAAGATCTACGAGATCTACCTCACAAGCTGCAAG 1620
Qy 1666 CCGGAAGACGTGAGGTGGCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATGTTAGC 1725
Db 1621 CCAGAAGACGTGAGGTGGCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATGTTAGC 1680
Qy 1726 TGTGGACCCCTCGCGCTCTGCTCACCCGCGCAGTCACTCTGGCTATGAGCACTGTGGG 1785
Db 1681 TGTGGGCCCCAGAGTCTGCTCACCCGCGCAGTCACTCTGGCAATGGAACCTGTGGA 1740
Qy 1786 GAGCCCAAGCCCTGACAGCTGGAGCTGCGCTCAAAAGCAGTCTGCGAGGGCAGCTGG 1845
Db 1741 GAGCCCAAGCCCTGACAGCTGGAGTCTGCGCTCAAAAGCAGTCTGCGAGGGCAGTGG 1800
Qy 1846 GAGGATGTGCTGACCTGGCGGAGGAGCGCTTCCACCTCTACTACTGCGAGCTGGAG 1905
Db 1801 GAGGATGTGCTGACCTTGTGTGAGGAGTCACTTCCACCTCTACTACTGCGAGCTGGAG 1860
Qy 1906 GCCAGTGCCTGCTACGCTTTCACCGAGCAGCTGGCGCGCTTGGCCCTGCTGCTGAGAGGCC 1965
Db 1861 GCCGGGCGCTGCTATGCTTTCAGGAGCAGCTGGCGCGCTTGGCCCTGCTGAGAGAGGCC 1920
Qy 1966 CTGAGCGTGGCTGCGCCCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCAAC 2025
Db 1921 CTGAGCGTGGCTGCGCCCAAGCGCTCAAGCGCTCCTTCTGTTTGTCTCCGCTGGCTGACG 1980
Qy 2026 TCCCTCGAGTACCAATCCGGGTCTACTGCTGCTGATGACACCCACGATGCACTCAAGGAG 2085
Db 1981 TCCCTTGAAGTACCAATCCGAGTGTACTGCTTACAGACACCCACGAGCTCTCAAGGAG 2040
Qy 2086 GTGGTGCAGCTGGAGAGCAGCTGGGGGAGCAGCTGATCAGGAGCCACGGGTCTCTGCAC 2145
Db 2041 GTGGTGCAGCTGGAGAGCAGCTAGGTGGACAGCTGATCAGGAGCCCTCGGCTCTGCAC 2100
Qy 2146 TTCAAGGACAGTTTACCAACCTTGCCTTATTCATCCAGATGTGCCAGCTCTCCTGTGG 2205
Db 2101 TTCAAGGACAGTTTACCAACCTTGCCTTATTCATCCAGCTCTCCTGCTGG 2160
Qy 2206 AAGAGTAACTCTTGTGCTGCTGAGGAGATCCCTTTTATCACATCTGGATGGCAGC 2265
Db 2161 AAGAGCAAGTCTTGTGCTGCTGAGGAGATCCCTTTTACCACTCTGGAACGGCACC 2220
Qy 2266 CAGCGGTACTTGCATCTGACCTTTCACCTGAGCGTGTGAGCCCGACACTAGTGAAGCTG 2325
Db 2221 CAGCAGTATCTGCACTGCACTTCACTCTGGAGGGATCAAGCGCAGCAACGAGCACTG 2280
Qy 2326 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGAAGGGCAGAGCTTTCAGCATCAACTTC 2385
Db 2281 GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCGAGAGCTTCAACATCAACTTC 2340
Qy 2386 AACATCAAGGACACAGGTTTGTGAGCTGTGCTGCTGAGGAGTGAAGCGGGGCTC 2445
Db 2341 AACATCAAGGACACAGGTTTGTGAAATTTGTGGCTCTGGAGAGTGAAGGGGGGCTC 2400
Qy 2446 CAGCCCTGTGTGGGCGCCAGTGTCTCAAGATCCCTTCTCATTTCCGCGAAGAGATAAT 2505
Db 2401 CAGCCCTGTGTGGGCGCCAGTGTCTCAAGATCCCTTCTCATTTCCGCGAAGAGATAAT 2460
Qy 2506 TCAGCCTGTGACCCACCTGTAGCGGGGTGCCGACTGGCGGACTCTGGCCCAAGAACTC 2565
Db 2461 GCCAGTCTGGACCCACCTGACGCCGGGGCGCAGTGGAGAACTCTAGCCCAAGAACTT 2520
Qy 2566 CACTGTGACAGCCATCTCAGCTTCTTGGCTTCCAGCCGAGCCCAAGCATGATCTC 2625
Db 2521 CACTGTGACAGCCATCTTACCTTCTTGGCTTCCAGCCGAGCCCTACAGCATGATCTC 2580
Qy 2626 AACCTGTGGGAGCGGCGCACTTCCCAACGGCAACTCAGCCAGCTGGCTGAGCAGCTG 2685
Db 2581 AACCTATGGAGGCAAGGCACTTCCCAACGGCAACTCAGCCAGCTGGCAGCAGCTG 2640
Qy 2686 GCTGTGAGCTGGGCGCAGCAGCTGCGCTCTTTCAGAGTGTGGAGGCTGAGTGTGA 2742

Db 958 CTGAGTACAACTCCGGGTCTACTGCTGATGACACCCACGATGCACTCAAGGAGTG 1017
Qy 2089 GTGAGCTGGAGAGAGCTGGGGGAGACGTGATCAGAGCCACGGGTCTTGCATTC 2148
Db 1018 GTGAGCTGGAGAGAGCTGGGGGAGACGTGATCAGAGCCACGGGTCTTGCATTC 1076
Qy 2149 AAGGACAGTTACCAACACCTTGGCCCTATCCATCCAGATGTGCCAGCTCCCTGTGAAG 2208
Db 1077 AAGGACAGTTACCAACACCT - -GCCCTATCATCCAGATGTGCCAGCTCCCTGTGAAG 1134
Qy 2209 AGTAAGCTCTTGTACCTACCAAGAGATCCCTTTTATCACATCTGGAATGGCAGCAG 2268
Db 1135 AGTAAGCTCTTGTACCTACCAAGAGATCCCTTTTATCACATCTGGAATGGCAGCAG 1194
Qy 2269 CGGTACTTGCACCTTCAACCTGGAGCGGTGTAGCCCCAGCACTAGTGAACCTGGCC 2328
Db 1195 CGGTACTTGCACCTTCAACCTGGAGCGGTGTAGCCCCAGCACTAGTGAACCTGGCC 1254
Qy 2329 TGCAGAGCTGTGGGTGGCAGGTGGAGGGGAGCGGCGAGAGCTTCAGCATCAACTTCAAC 2388
Db 1255 TGCAGAGCTGTGGGTGGCAGGTGGAGGGGAGCGGCGAGAGCTTCAGCATCAACTTCAAC 1314
Qy 2389 ATCAACAGGACACAAAGTTTGTGAGCTGTGCTGCTCTGGAGAGTGAAGCGGGTCCCA 2448
Db 1315 ATCAACAGGACACAAAGTTTGTGAGCTGTGCTGCTCTGGAGAGTGAAGCGGGTCCCA 1374
Qy 2449 GCCGTGTGGGCCCCAGTGTTCAGATCCCTTCTCATTCGGGAGAGATAAATTTCC 2508
Db 1375 GCCGTGTGGGCCCCAGTGTTCAGATCCCTTCTCATTCGGGAGAGATAAATTTCC 1434
Qy 2509 AGCTTGAGACCCACCTGTAGCGGGGTGGCGAGCTTGGCGGAGCTTGGCCAGAACTCCAC 2568
Db 1435 AGCTTGAGACCCACCTGTAGCGGGGTGGCGAGCTTGGCGGAGCTTGGCCAGAACTCCAC 1494
Qy 2569 CTGGACAGCCATCTCAGTCTTTTGGCTTCAAGCCAGCCAGCCAGCCATGATCCTCAAC 2628
Db 1495 CTGGACAGCCATCTCAGTCTTTTGGCTTCAAGCCAGCCAGCCAGCCATGATCCTCAAC 1554
Qy 2629 CTGTGGAGGGGGGCACTTCCCAACGGCAACCTCAGCCAGCTGGGTGACGAGTGGCT 2688
Db 1555 CTGTGGAGGGGGGCACTTCCCAACGGCAACCTCAGCCAGCTGGGTGACGAGTGGCT 1614
Qy 2689 GGACTGGCCAGCCAGAGCTGGCTTCTTTCACAGTG -TTCACAGTG -TCGGAGGCTGAGTGTGGGCC 2746
Db 1615 GGACTGGCCAGAGGAGCTGGCTTCTTTCACAGTGTTCCGAGGCTGAGTGTGGGCC 1674
Qy 2747 GGCCAG 2752
Db 1675 GGCCAG 1680

RESULT 12

US-10-296-115-365
; Sequence 365, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hypeq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552, 317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 365
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-365

Query Match

43.8%; Score 1206.6; DB 18; Length 1321;

Best Local Similarity 98.0%; Pred. No. 1.4e-299;
Matches 1295; Conservative 0; Mismatches 19; Indels 7; Gaps 7;
Qy 1435 CACACACTGCACACAGCTCTCCACCTCTAGAGCCGAGGAGTTCGTCTCCGCTCTCC 1494
Db 1 CACACACTGCACACAGCTCTCCACCTCTAGAGCCGAGGAGTTCGTCTCCGCTCTCC 60
Qy 1495 ACCAGAACTACTTTCGCTCCCTGCCCCGAGGCAACAGCAAAATGACCTTATGGACCTTC 1554
Db 61 ACCAGAACTACTTTCGCTCCCTGCCCCGAGGCAACAGCAAAATGACCTTATGGACCTTC 120
Qy 1555 AACTTCTCGGGGGCGGTGATGATCCCTAATACAGGTATACGCTCTCATCCCCCA 1614
Db 121 AACTTCTCGGGGGCGGTGATGATCCCTAATACAGGTATGACCTCTCATCCCCCA 180
Qy 1615 GATGCATACCCCCGAGGAAAGATCTATGAGATCTAGCTCACGCTGACAAAGCCGGAAGAC 1674
Db 181 GATGCATACCCCCGAGGAAAGATCTATGAGATCTACTCACGCTGACAAAGCCGGAAGAC 240
Qy 1675 GTGAGTTGCCCCCTAGCTGGCTGTACAGCCCTGCTGAGTCCCATGTTAGCTGTGACCC 1734
Db 241 GTGAGTTGCCCCCTAGCTGGCTGTACAGCCCTGCTGAGTCCCATGTTAGCTGTGACCC 300
Qy 1735 CCT -GGCGTCTGCTCACCGGCCAGTCACTCT -GGCTATGGACCACTGT -GGGGAGCCC 1791
Db 301 CCTGGGGCTGCTCTGTTACCGGCCAGTCACTCTGGGGTATGGAACCTGTGGGGAGCCC 360
Qy 1792 AGCCCTGACAGCT -GGAGCTGCGCTCAAAAAGCAGTCTGTGCGAGGCGAGCTGGGAGGA 1850
Db 361 AGCCCTGACAGCTGGGAGCTGCGCTCAAAAAGCAGTCTGTGCGAGGCGAGCTGGGAGGA 420
Qy 1851 TGTGCTGACCTGGGGGAGAGCGCCCTCCACCTCTACTACTGCGAGCTGAGGCGCAG 1910
Db 421 TGTGCTGACCTGGGGGAGAGCGCCCTCCACCTCTACTACTGCGAGCTGAGGCGCAG 480
Qy 1911 TGCCTCTAGCTCTTCCACGAGCAGCTGGCGCGCTTTTGCCTCTGTTGGGAGAGCCCTCAG 1970
Db 481 TGCCTCTAGCTCTTCCACGAGCAGCTGAGCCCTATGCCCCGTGTTGGGAGAGCCCTCAG 540
Qy 1971 CGTGGCTGCGCCCAAGCGCTCAAGCTGCTTGTGTTTGGCCCGGTGGCTGCACTCCCT 2030
Db 541 CGTGGCTGCGCCCAAGCGCTCAAGCTGCTTGTGTTTGGCCCGGTGGCTGCACTCCCT 600
Qy 2031 CGAGTACACATCCGGGTCTACTGCTGATGACACCCAGATGCACTCAAGAGTGGT 2090
Db 601 CGAGTACACATCTGCTCTACTGCTGATGACACTCAAGATGCACTCAACCTAGTGGT 660
Qy 2091 GCAGCTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCCACCGGTCTCTGCACTTCAA 2150
Db 661 GCAGCTGGAGAGCAGCTGCGAGGACAGCTGATCCAGGAGCCACTGGTACTGCACTTCAA 720
Qy 2151 GGAAGTTACCAACACTGCGCTATCCATCCAGATGTGCCAGCTCTCTGTGGAAGAG 2210
Db 721 GGAAGTTACCAACACTGCGCTATCCATCCAGATGTGCCAGCTCTCTGTGGAAGAG 780
Qy 2211 TAGCTCTGTGCTGCTGAGAGATCCCTTTTATCATCTGGAATGGAGCGAGCG 2270
Db 781 TAGCTCTGTGCTGCTGAGAGATCCCTTTTATCATCTGGAATGGAGCGAGCG 840
Qy 2271 GTACTTGCACCTGCACTTCACTGAGGCTGTGACGCCCGCAGCACTAGTACCTGGCGCTG 2330
Db 841 GTACTTGCACCTGCACTTCACTGAGGCTGTGACGCCCGCAGCACTAGTACCTGGCGCTG 900
Qy 2331 CAAGCTGTGGGTGTGAGGCGGAGCGGCGAGCTTCAAGATCAACTTCAACAT 2390
Db 901 CAAGCTGTGGGTGTGAGGCGGAGCGGCGAGCTTCAAGATCAACTTCAACAT 960
Qy 2391 CACCAAGGACACAAAGTTTGTGCTGAGCTGCTGGAGTGAAGCGGGGTCCAGC 2450
Db 961 CACCAAGGACACAAAGTTTGTGCTGAGCTGCTGGAGTGAAGCGGGGTCCAGC 1020
Qy 2451 CTTGTGGGGCCCGAGTGGCTTCAAGATCCCTTCTCATTCGGCAGAGATAATTTCCAG 2510

Db 1021 CCTGGTGGCCCCAGTGCCTTCAAGATCCCTCTCTCAATCGGCAGAGATAATTTCCAG 1080
Qy 2511 CCTGACCCACCTCTGTAGGGGGTGGCGACTGGCGACTCTGSCCCAGAAACTCCACCT 2570
Db 1081 CCTGACCCACCTCTGTAGGGGGTGGCGACTGGCGACTCTGSCCCAGAAACTCCACCT 1140
Qy 2571 GGACAGCCATCTCAGCTTCTTTGCTCTCAAGCCCGAGCCCCACAGCCCATGATCTCAACCT 2630
Db 1141 GGACAGCCATCTCAGCTTCTTTGCTCTCAAGCCCGAGCCCCACAGCCCATGATCTCAACCT 1200
Qy 2631 GTGGAGCGCGGCGACTCTCCCAAGCGCAACCTCAGCGAGCTGGCTCAGAGTGGCT-G 2689
Db 1201 GTGGAGCGCGGCGACTCTCCCAAGCGCAACCTCAGCGAGCTGGCTCAGAGTGGCTGG 1260
Qy 2690 GACTGGGCGCAGCAGACGCTGGGCTC-TTACAGTG-TCCGAGGCTCAGTGGCTGAGGCCG 2747
Db 1261 GACTGGGCGCAGCAGAGCGTGGCTCTTTACAGTGTTCGAGGCTCAGTGGCTGAGGCCG 1320
Qy 2748 G 2748
Db 1321 G 1321

RESULT 13

us-10-087-684-1

; Sequence 1, Application US/10087684

; Publication No. US20040029116A1

GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Caaman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Balog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-1

Query Match 34.0%; Score 936.2; DB 17; Length 2860;
Best Local Similarity 61.7%; Pred. No. 4.1e-230;
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

Qy 143 ACCAGTGCCTGTGTCACACCCCGAGACTGTCTCCCACTTCTCTGTGGAGCCCGAGAGATG 202
Db 168 ACTCTCTCCGTGAGCGCCAGCAGAGCGCTGCCCTACTTCTCTGAGAGCCACAGAGCG 227
Qy 203 TGTACATCGTCAAGAAACAAGCCAGTGTCTGTGTGCAAGGCCGTGCCCGCCACAGCA 262
Db 228 CCTACATTTGGAAGAAACAAGCTGTGTGAGCTCCGCTGCCGCGCTTCCCCGCCACAGCA 287
Qy 263 TCTTTCTTCAAGTCAACGGGGAGTGGGTGCGCCAGGTGGACCAACGTCGATCGAGCGCAGCA 322
Db 288 TCTACTTCAAGTCAACGGCGAGTGGGTGAGCCAGAAACGACACGCTCACACAGAGAGGCC 347
Qy 323 CAGACGGAGCAGTGGGCTGCCCAACATGAGAGTCCGCATTAATGTCTCAAGGAGAGAGG 382
Db 348 TGGATGAGGCCACCGGTCTGCGGGTGGCGAGGTGCAGATCGAGGTGTTCGCGGAGCAGG 407
Qy 383 TCCAGAGAGTGTTCGGGCTGGAGGAATACTGTGCCAGTGCCTGGCATGAGGCTCTCTCGG 442
Db 408 TGGAGGAGCTCTTTGGGCTGGAGGAATTAATGTGTGCCAGTCCGTGGCTTGGAGCTCCCGG 467
Qy 443 GCACCAACAGAGTCAAGAGCGCTTACATCCGCATAGCCAGATTTCGCAAGAACTTCGAGC 502
Db 468 GCACCAACAGAGTCCGCCGAGCTTACGTCCGCATCGCTTACCTGCGCAAGACTTCGATC 527
Qy 503 AGAGCGCGTGGCCAAAGAGGTGTCTCCGTGAGAGAGGAGCATCTGTGCTGCCCTGCCGTCAC 562
Db 528 AGGAGCTCTTGGGCAAGAGAGGTGCCCTTGGACCATGAGGTTCCTCTGAGTGGCGCCGC 587
Qy 563 CGGAGGGCATCCCTCCAGCGGAGTGGAGTGGCTCCGGAAACGAGGACCTGCTGTGACCCGT 622
Db 588 CGAGGGGGTGCCTGTGGCGAGTGGATGGCTCAAGATGAGGATGTCTATGACCCCA 647
Qy 623 CCTGGAGCCCAATGTATATCATCACGGGGAGCAGACCTGTGTGTGTCGACAGGCCCGCC 682
Db 648 CCAGAGCACCACCTTCTCTGCTCACCATCGACCAACCTCATCATCCGCGAGCCCGCC 707
Qy 683 TTGCTGACAGCGCCAACTACCTGTGTGCGCAAGAACATCTGTGGACAGTGTGCGGAGAGG 742
Db 708 TGTGCGACACTGCAACTATACCTGTGTGCGCAAGAACATCTGTGGCCAAACGCGGAGCA 767
Qy 743 CTTCCGCTGTGTCTATCTGTCTAGTGAACGGTGGTGGTGCAGCTGGACCGAGTGTGCTCG 802
Db 768 CCACTGCCCGTCTATCTGTCTAGTGAATGGCGGTGGTCCAGCTGGGCGAGAGTGTGTAC 827
Qy 803 TCTGACAGCGCAGCTGTGTGGCGCGGTGTGGCAGAAACGGAGCCGGAGCTGCACCAACCCG 862
Db 828 CCTGCTCCAAACCGCTGTGTGGCGAGGCTGGCAGAGCGCACCCCGAGCTGCACCAACCCG 887
Qy 863 CGCTCTCAACGGGGGGCTTTCTGTGAGGGGGAGAAATGTTCAGAAAAACAGCTTGCGCCA 922
Db 888 CTCACTCAACGGAGGGGGCTTCTGTGCGAGGGCCAGGCAATTCACAGAGAGACCGCTGCAACA 947
Qy 923 CCCTGTGCCAGTAGACCGCAGCTGGAGCCCGTGGAGCAAGTGTGCGGCTGTGGGCTGG 982
Db 948 CCACTGTGCCAGTTCGATGGGGCGTGGAGTGGAGCAAGTGTTCAGCTTCGACGACTG 1007
Qy 983 ACTGCACCCCACTGGCGAGCGTGTAGTGTCTGTACCCAGCACCCCGCAACCGAGGGAGG 1042
Db 1008 AGTGTGCCCACTGGCGTAGCGGAGTGTGATGCGCGCCCCCAGAGACGGAGGGCGTG 1067
Qy 1043 AGTGCAGGGGCACTGACCTTGGACACCCCGCAACTGTATACAGTGTACCTCTGTGTACAGTG 1102
Db 1068 ACTGCAGCGGAGCGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGTGATCAACTGG 1127

Qy	1103	CTTCTGGCCCTGAGGAGTGCGCCCTCTATGTGGGCTCATCGCGTGGCGGTCTGCCTGG	1162
Db	1128	AGGCTTCAGGGGATGCGGCGCTGTATGCGGGCTCTGTGTGGCCATCTTCTGTGTCTGTG	1187
Qy	1163	TCCTGTCTCTTGTCTCTCATCTCTGTATTATGCGGAGAAAGGAGGGCTGTGACTCAG	1222
Db	1188	CAATCTCTATGCGGTGGGGTGTGTATCCGCCGAATCTGCCGTCTTCTGACACAG	1247
Qy	1223	ATGTGGTGACTCTGTCAATT---CTCACTCAGGCTTCCAGCCCGTCTGACATCAAGCCCA	1279
Db	1248	ACATCACTGACTCATCTGCTGCCCTGACTGTGTGTTTCCACCCCGTCAACTTTAAGACGG	1307
Qy	1280	GCAAGCAGACAAACCCCATCTGCT-----CACCATCTGAGCCGGAGCTCAGCACCA	1333
Db	1308	CAAGGCCAGTAAACCGGAGCTCTACACCCCTCTGTGCTCTCTGACTCAGACCCAGCG	1367
Qy	1334	CCACCACCTACAGGGGAGTCTCTGTCCCGGAGGA-----	1370
Db	1368	CCGCACTACCGCGGACCCGTGTATGCTCTGACGAGTCCACCGACAAATCCCATGA	1427
Qy	1371	-----TGGGCGCAGCCCAAGTTCAGCTCACCA-----	1399
Db	1428	CCAACTCTCTCTCTGCTGGAACCCCTTACCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA	1487
Qy	1400	--ATGGGCACCTGTCTAGACCCCTCTGGTGGCGCGCCACAC-----ACTGCACC	1447
Db	1488	CCAGGGCTCTGGGCGAGGCTGCGCATATGGGCTGACCTGTGGGGTCTTGGCGCTG	1547
Qy	1448	ACAGCTCTCCCACTCTGAGGCGAGGAGTTGCTCTCCCGCTTCCACCCAGAACTACT	1507
Db	1548	GCACATACCTTAGCGATTCTGCCCGGACACCACTTCTTGCACTCGCGAGCGCCAGCC	1607
Qy	1508	TCCGCTC-----CCTGCCCGAGGCAACGACATGACCTATGGGACCT	1552
Db	1608	TCGGTTCCTCAGAGCTCTGGGCTGCCCCGAGACCCAGGAGCAGGCTCAGCGGACCT	1667
Qy	1553	TCAACTTCTCGGGGGCGGCTGATGATCCCTAATACAGGTATCAGGCTCTCATCCCCC	1612
Db	1668	TTGGCTGCTGGTGGGAGCTCAGCATCCCGSCACAGGGGTCTGCTGTGTGCCCA	1727
Qy	1613	CAGATGCCATACCCGAGGAGAGATCTATGAGTCTACTCAAGCTGCAACAGCGGAG	1672
Db	1728	ATGAGGCAATCCCCAGGGCAAGTTCTACAGATGTATCTACTCATCAACAGAGCAGAAA	1787
Qy	1673	ACGTGAGGTGCCCTAGCTGGCTGTCTAGACCCCTGCTGAGTCCCATCGTTAGTGTGGAC	1732
Db	1788	GTACCTGCCGCTTTCAGAGGACCCAGACAGTATTAGCCCTCGGTGACCTGTGGAC	1847
Qy	1733	CCCTGGGCTCTGCTCACCGGCGATCTATCTGTGGTATGAACTGTGGGAGGCCCA	1792
Db	1848	CCAGAGCCTCTCTGTGCGGCCCTCATCTCTCACCATGCCCACTGTGCGGAGTCA	1907
Qy	1793	GCCCTGACAGCTGGAGCTCGGCTCAAAAGCAGTCTGCGAGGGCAGCTGGAGGATG	1852
Db	1908	GTGCCGTGACTGGATCTTTTTCAGTCAAGACCCAGGCCCACTGGAGGAGG	1967
Qy	1853	TGCTGCACCTGGGCGAGGAGCGCCCTCCACCTCTACTATGTCAGCTGGAGGCCAGTG	1912
Db	1968	TGGTGAACCTGGATGAGGAGACCTGAACACACCTCTACTGTCAGCTGGAGGCCAGGG	2027
Qy	1913	CCTGCTACGTTTACCGAGCAGTGGGCGGCTTTGGCCCTGTGGGAGAGGCCCTCAGCG	1972
Db	2028	CCTGTCACTCTGCTGGAACAGCTGGGACCTTACGTTTTCAGGGCGAGTCTTATTC	2087
Qy	1973	TGGCTGCGCCCAAGCGCTCAAGCTGCTTCTGTTTGGCGGCTGGCCTGCACTCCCTCG	2032
Db	2088	GCTCAGCAGTCAAGCGCTCCAGTGGCGCTTCTGCGCCCGCCCTCTGCACTCCCTG	2147
Qy	2033	AGTACAACATCCGGGTCTACTGCTGTGATGACCCACAGATGACCTCAAGAGGAGTGTGC	2092
Db	2148	AGTACAGCTCCGGGTCTACTGCTGTGAGGACAGCCCTGTAGCACTGAAGAGGAGTGTG	2207

QY	2093	AGCTGGAGAGACAGCTGGGGGGA	CAGCTGATCAGGAGGCCACGGGTCTCTGCAC	TTCAAGG	21515	
Db	2208	AGCTGGAGCGGACTCTTGGGGGGA	TACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG	22677		
QY	2153	ACAGTTACCAACAACCTCGCTTATCCAT	CACGATGTGCCAGCTCCCTCTGTGGAAGAGTA	22112		
Db	2268	ACAGTTACCAACAACCTCGGCTCTCCCTCCAT	GAACCTCCCATGCCCATTGGAGGAGCA	23277		
QY	2213	AGCTCCTTGTCAAGCTACCAAGAGATCCCC	TTTATCACATCTGGAATGGCACGACGGT	22727		
Db	2328	AGCTGCTGGCCAAATACACAGAGATCCCC	TTCTATCACATTTGAGTGGCAGCCAGAAGG	23877		
QY	2273	ACTTGCACCTGACCTTCAACCTGGAGGGTGT	CAGCCCCAGCACATCTAGTGAACCTGGCCCTGCA	23332		
Db	2388	CCCTCCCACTGCACTTTTCAACCTGGAGAGG	CACAGCTTGGCCCTCCACAGAGCTCACCTTGCA	24477		
QY	2333	AGCTGTGGGTGTGGCAGGTGGAGGGCGAC	GGGGCAGAGCTTTCAGCATCAACTTCAACATCA	23927		
Db	2448	AGATCTCGTGGCGAAGTGGAGGGGAGGGC	CAGATATTTCCAGCTGCATACCACCTCTGG	25077		
QY	2393	CCAAG----	GACACAGGTTTTGCTGAGCTGTCTGGCTCT	GTGAGAGATGAAGCGGGGTGCCAG	24497	
Db	2508	CAGAGACACCTGTCTGCTCCCTGGACACT	CTCTGCTCTGCCCCCTGGCAGCACCTGTCA	25677		
QY	2450	CCCTGTGGGCGCCAGTGGCTTCAAGATCCCC	TTCTCATTTGGGCAGAAATATTTCCA	25097		
Db	2568	CCAGCTGGGACCTTATGCTTCAAGATCCCA	CTGCTCCATCCGCCAGAGATATGCAACA	26277		
QY	2510	GCCTGGACCAACCTGTAGCGGGGTGCCAG	CTGGGGGACTCTGGGCCAGAACTCCACC	25697		
Db	2628	GCCTAGATGCCCCCAACTCAACGGGGCAAT	GACTGGGGGATGTTAGCACAGAACTCTCTA	26877		
QY	2570	TGGACGCCATCTCAGCTTCTTTGGCTTCC	AAAGCCAGCCCAAGCATGTATCCTCAACC	26297		
Db	2688	TGGACCGGTACCTGAATTCTTTGCCACCA	AAAGCGAGCCCAAGGTGTATCCTGGACC	27477		
QY	2630	TGTGGGAGGGCGGCACTTCCCAACGGCAAC	CTCAGCCAGCTGGCTGCGACGAGTGGCTG	CAGCAGTGGCTG	26897	
Db	2748	TCTGGGAAGCTCTGCAGCAGGACGATGGG	AGCCTCAACAGCCTGGCGAGTGCCTTGAGG	28077		
QY	2690	GACTGGGCCAGCAGCGCTGGCCCTTTCAC	AGTGTGGAGGCTGAGTGTCTGA	2742		
Db	2808	AGATGGGCAAGAGTGAGATCGTGGTGTG	CGCCACCGAGGGGAGTCTCTGA	2860		

RESULT 14

US-10-087-684-3

; Sequence 3, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Caaman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.

APPLICANT: Gangolli, Esha A.
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-214 CIP

CURRENT APPLICATION NUMBER: US/10/087,684

CURRENT FILING DATE: 2003-03-10

PRIOR APPLICATION NUMBER: 60/253,834

PRIOR FILING DATE: 2000-11-29

PRIOR APPLICATION NUMBER: 60/250,926

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: 60/264,180

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 60/274,194

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 60/313,656

PRIOR FILING DATE: 2001-08-20

PRIOR APPLICATION NUMBER: 60/327,456

PRIOR FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 220

SOFTWARE: CuraSeqlist version 0.1

SEQ ID NO 3

LENGTH: 2860

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (59)..(2857)

US-10-087-684-3

Query Match 34.0%; Score 936.2; DB 17; Length 2860;

Best Local Similarity 61.7%; Pred. No. 4.1e-230;

Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

143 ACCAGTGCCTGGTCCCAACCGGACCTGCTTCCCTCCCTCTCTGCTGGAGCCCGGAGTG 202
168 ACTCTTCCCTGTCAGCGCAGCAGCGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 227
203 TGATACATCGTCAAGAACAAAGCAGTGTCTGTGTGCAAGCGCTGCTGCTGCTGCTGCTG 262
228 CCTACATTGTGAAGAACAAAGCAGTGTCTGTGTGCAAGCGCTGCTGCTGCTGCTGCTG 287
263 TCTTCTTCAAGTCAAGCGGAGTGGGTGCGCCAGGTGACACAGTGTGACGAGCGCAGCA 322
288 TCTACTTCAAGTCAAGCGGAGTGGGTGACGACGAGAACGACGACGACGACGACGACG 347
323 CAGACGGGAGCAGTGGGCTGCCACCATGGAGTCCCGATTAAATGCTCAAGCGACGAG 382
348 TGGATGAGGACACCGGCTGCGGCTGCGGAGTGGCAGATCGAGGTGTGCGGCGAGCAG 407
383 TCGAAGAGGTGTTTCGGGCTGAGGAATATCTGGTGCCAGTGGTGGCAATGGAGCTCTCTCG 442
408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGGTGGCTGGAGCTCCGAG 467
443 GCACCAAGAGTCAAGAGCCTACATCGGCATAGCAGATTCGCGCAAGAACTTCGAGC 502
468 GCACCAAGAGTTCGCGGAGCTACGTCGCGCATCGCTTACCTGCGCAAGAACTTCGATC 527
503 AGGAGCGCTGGCCAAAGAGTGTCCCTGGAGCAGGCGCATCGTCTGCTGCTGCTGCTGCT 562
528 AGGAGCTCTGGGCAAGAGTGTCCCTGGACCAATGAGGTTCCTCTGAGTGGCGCGCCG 587
563 CGGAGGCGCATCTCTCCAGCGAGTGGAGTGGCTTCCGGAACGAGGACCTGGTGGACCCGT 622
588 CGGAGGCGGTGCTGTGGCGGAGTGGAAATGGCTCAAGATGAGGATGTCATCGACCCCA 647
623 CCTTGGACCCCAATGATATACATACGCGGAGCAGACGCTGGTGGTGGAGCAGCGCCG 682
648 CCGAGGACACCAATCTCTGCTTACCATCGACCAACAACTCATCATCGCGCAGGCGCCG 707
683 TTGCTGACAGCGGCAATACACCTGCTGGCCAGACATCGTGGCAGCTGCGCGAGCG 742
708 TGTGGACATGCGCAACTATACCTGCTGGCGCAAGAAACATCGTGGCGCAAGCGGAGCA 767
743 CCTCCGCTGTCTATCGTCTACGTGAACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 802

Db 768 CCACTGCCACCGTCTACGTGAATGGCGCTGGTCCAGTGGGCGAGTGGTCCAC 827
Qy 803 TCTGACGCGCAGCTGTGGGCGCGGCTGGCAGAAACGAGCGGAGTGTGACCAACCGG 862
Db 828 CTTGCTCCAAACCGCTGTGGCGGAGCTGGCAGAGCGCACCGGACCTGACCAACCGG 887
Qy 863 CGCTCTCAACGGGGCGCTTCTGTGAGGGGAGAGATGTCAGAAACAGACCTGCGGCA 922
Db 888 CTCACACTCAACGGAGGGGCTTCTGCGAGGGGCGAGGATTCAGAGAGACCGCTGCA 947
Qy 923 CCTGTGCTCCAGTAGACGCGAGCTGGAGCCCGTGGAGCAAGTGTGCGGCTGTGGCTG 982
Db 948 CCATGCTCCAGTCGATGGGCGCTGGACGAGTGGAGCAAGTGTGACGCTGACGACTG 1007
Qy 983 ACTGACCCCACTGGCGAGCGTGTGCTGTCTGACCGAGCAACCGGCAAGAGGGGAG 1042
Db 1008 AGTGTGCCACCTGGCGTAGCGGAGTGCATGCGCGCCCGCCACCCAGAGGAGCGGTG 1067
Qy 1043 AGTGCCAGGCGACTGACCTGACACCGCAACTGTACCACTGACCTGTGTACACAGTG 1102
Db 1068 ACTGACGCGGACGCTGCTGCACTCTAAGAACTGCACAGATGGGCTGTGATGCACTG 1127
Qy 1103 CTTTGTGCGCTGAGGAGCTGGCCCTCTATGTGGGCGCTCATCGCGTGGCGCTGTGCTG 1162
Db 1128 AGGCTCAGGGGATGCGGCGCTGTATGCGGCGCTGCTGTGGCCATCTTCTGTGCTG 1187
Qy 1163 TCTGTGCTGTGCTGTCTCATCTCTGTTTATGTCGCGAAGAGGAGGGGTGAGCTCAG 1222
Db 1188 CAATCTCTCATGGCGGTGGGTGTGTACCGCGCGCAACTGCGGTGACTTTCGACACAG 1247
Qy 1223 ATGTGCTGACTCGTCCATT---CTACCTCAGGCTTCCAGCGCGCTGACGATCAAGCC 1279
Db 1248 ACATCTGACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1307
Qy 1280 GCAAGCAGACAAACCCCATCTGCT-----CAACATCCAGCGGAGCTCAGCACCACCA 1333
Db 1308 CAAGGCGCAGTAACCGCGAGCTCTACACCCCTCTGTGCTCTGCTGCTGCTGCTGCTG 1367
Qy 1334 CACACCATACAGAGGAGTGTCTGTCTCCCGGAGCA----- 1370
Db 1368 CCGGCACTACCGCGGACCGGTGTATGCTGCTGAGGACTCCACCGCAAAATCCCCATGA 1427
Qy 1371 -----TGGGCGCAGCGCCCAAGTTCAGCTCACA----- 1399
Db 1428 CCAACTCTCTGCTGAGACCCCTTACCCAGCTTAAAGTCAAGGTCTACAGTTCAGCA 1487
Qy 1400 --ATGGGCACTGCTCAGCCCTCTGGGTGGCGCGCGCACAC-----ACTGCACC 1447
Db 1488 CCAAGGCTCTGGGCGCAGGCTGGCAGATGGGCGTGCACCTGCTGGGGGTCTTGGCGCTG 1547
Qy 1448 AGAGCTCTCCACCTGTAGAGCGGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1507
Db 1548 GCACATACCTTAGCGATTTGGCGCGGACACCCACTTCTCTGACCTGCGAGCGGCGC 1607
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Qy 1553 TCAACTTCTCTGGGCGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCTCATCCCC 1612
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Qy 1613 CAGATGCCATACCCCGAGGAGAGATCTATGAGATCTATCTCAGCTGCGACAGCGGAG 1672
Db 1728 ATGGAGCCATATCCCGAGGCGAGTCTTACGAGATGTATCTACTCATCAACAGGCGA 1787
Qy 1673 ACGTGAGTTGCCCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1732
Db 1788 GTACCTCGCGCTTTCAGAGGAGGACCCAGACAGTATTTGAGGCGCTCGGTGACTGTG 1847
Qy 1733 CCCTCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1792

Db 1848 CCACAGGCTCTCTGTGCGGCCCGCTCATCTCTCACCATGCCCCACTGTGCGCAAGTCA 1907
Qy 1793 GCCTGTGACAGTGTGAGCTTGGCTCTCAAAAGCAGTGTGTCGAGGGCAGCTGGAGGAGT 1852
Db 1908 GTGCCCGTGAAGTGTCTTTGAGTCAAGACCCAGGCCCCACAGGGCCACTGGGAGGAG 1967
Qy 1853 TGTGTGACCTTGGGAGGAGGCGCCCTCCACCTCTACTACTGCGAGTGTGAGGCCAGTG 1912
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Qy 1913 CCTGTACGTCTTCCACGAGCAGCTGGGCGGCTTTGGCCCTGTGGTGGGAGAGGCCCTCAGCG 1972
Db 2028 CCTGTACATCTCTGTGACAGCTGGGACCTACGTGTTCACGGGCGAGTCTATTCCC 2087
Qy 1973 TGGTGTGCGGCAAGCGCTCAAGTGTCTTGTGTTGGCGCGGTGGCTGCACTTCCCTCG 2032
Db 2088 GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGCTCTTGGCCCCGCCCTCTGCACCTCCCTGG 2147
Qy 2033 AGTACACATCCGGGTCTACTGCTGTGATGACACCCACGATGCACTCAAGGAGTGTGTC 2092
Db 2148 AGTACAGCTCCGGGTCTACTGCTGTGAGGACAGCGCTGTAGCACTGAAGGAGTGTGTCG 2207
Qy 2093 AGCTGGAAGACAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCTCTGCACTTCAAGG 2152
Db 2208 AGCTGAGCGGACTCTGGGCGGATCTTGTGTGAGGAGCCGAAACCGCTAATGTTCAGG 2267
Qy 2153 ACAGTTACCAACACTGGGCTATCCATCCACGATGTGCCAGTCCCTGTGGAAGATTA 2212
Db 2268 ACAGTTACCAACACTGGGCTCTCCCTCCATGACCTCCGCCATGCCCCTTGGAGGAGCA 2327
Qy 2213 AGCTCTGTGTGACGTACAGGAGATCCCTTTTATCAGATCTGGAATGGCACCGGCT 2272
Db 2328 AGCTGTGGGCAATACAGGAGATCCCTTCTATCATACTTGGAGTGGCAGCAGAGG 2387
Qy 2273 ACTTGCACTGACCTTCCACCTGTGAGGCTGTGAGCCCGACACTAGTGAAGCTGGCTGCA 2332
Db 2388 CCCTCCACTGCACTTTTCACTTGGAGAGGACAGCTTGGGCTCCACAGAGCTCACCTGCA 2447
Qy 2333 AGCTGTGGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2392
Db 2448 AGATCTGCTGTGCGGCAAGTGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2507
Qy 2393 CCAAG---GACAAAGGTTGCTGAGCTGTGCTGTGCTGTGAGAGTGAAGCGGGGTCCAG 2449
Db 2508 CAGAGAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2567
Qy 2450 CCCTGTGGGCCCCAGTGTCTTCAAGATCCCTTCTCTTCAATTCGCGCAGAGATTAATTCCA 2509
Db 2568 CCAGCTGGGACCTTATGCTTCAAGATCCCACTGTCCATCCGCCAGAGATATGCAACA 2627
Qy 2510 GCCTGGACCCACCTGTAGGGGGGTGCGGACTGGGCGGACTTGGGCCAGAAACTCCACC 2569
Db 2628 GCCTAGATGCCCCCAACTCAAGGGGCAATGACTGGCGGATGTAGCACAGAAGCTCTCTA 2687
Qy 2570 TGAGACGCACTCAGCTTCTTGGCTTCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 2629
Db 2688 TGAGACCGTACCTGAATTAATTTTGGCAACAAAGGAGGAGGAGGAGGAGGAGGAGGAG 2747
Qy 2630 TGTGGGAGGCGGCACTTCCCAAGCGCAACCTCAGCCAGCTGGCTGTCAGAGTGTGCTG 2689
Db 2748 TCTGGGAAGCTCTGACAGGAGAGTGGGAGCTTCAACAGCTTGGCGAGTGTGAGG 2807
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Db 2808 AGATGGGCAAGAGTGAAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2860

RESULT 15

US-10-218-779-1

; Sequence 1, Application US/1021879

; Publication No. US2004002922A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit

; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangoli, Bsha
; FILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-218-779-1

Query Match 34.0%; Score 936.2; DB 17; Length 2860;
Best Local Similarity 61.7%; Pred. No. 4.1e-230;
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;
Qy 143 ACCAGTGTCTGTGTGCAACCCCGACCTGTCTCCCACTTCTCTGTGGAGCCCGAGGATG 202
Db 168 ACTCTCTCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 227
Qy 203 TGTACATGTCAAGAACAGCCAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 262
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Qy 263 TCTTCTTCAAGTGTCAACGGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 322
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Qy 323 CAGACGGGAGCAGTGTGGGCTGTGCCACCATGTGAGGTTCGCAATTAATGTCTCAAGGCGAGG 382
Db 348 TGGATCAGGCCACCCGCTCTGCGGGTGTGCGAGGTGTGAGGTGTGCGCGCAGCAGG 407
Qy 383 TCGAGAGGCTGTTCGGGCTGTGAGGAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 442
Db 408 TGGAGGAGCTCTTTTGGGCTGTGAGGAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 467
Qy 443 GCACCACCAAGAGTCAAGAGGCTTACATCCGATAGCCAGATTGCGCAAGAACTTTCGAGC 502

Db 468 GCACACCAAGAGTCGCGAGCCTACGTCGCGCTACGTCGCGAAGAACTTCGATC 527
 Qy 503 AGGAGCCCTCGCCCAAGAGGTGTCCTTGGAGCAGGCGATCGTGTGCTCCCTGCGGTCCAC 562
 Db 528 AGGAGCCTCTGGGCAAGAGGTGCGCCCTGSGACCAATGAGGTTCTCTTCGAGTGCCTGCGC 587
 Qy 563 CGGAGGGCAATCCCTCCAGCCGAGGTGAGTGGCTCGGAAGCAGAGACTGTGTGACCCGT 622
 Db 588 CGGAGGGGTGCTGTGGCCGAGGTGAGATGGCTCAAGATGAGGATGTCAATGACCCCA 647
 Qy 623 CCCTGGACCCCAATGTATATACATCAGCGGGAGCAAGCTGGTGGTGGCAGAGCCCGCC 682
 Db 648 CCCAGGACACCAACTTCTGCTCACCACCGACCAAACTCATCCGCGAGCCCGCC 707
 Qy 683 TTGTGTACACGGCCCACTACACTCGCTGGGCGCAAGACATCGTGCAGCTGCGCGCAGCG 742
 Db 708 TGTGGGACACTGCGCAACTATACCTGCGTGGGCGCAAGAACATCGTGGCCCAAGCGCGAGCA 767
 Qy 743 CCTCGCTGTGTATCGTCTACGTGAACGGTGGTGGTGCAGCTGGACCGAGTGGTCCG 802
 Db 768 CCATGCGCACCGTATCGTCTACGTGAATGGGCTGGTGCAGCTGGGAGAGTGGTCCAC 827
 Qy 803 TCTGAGCGCCAGCTGTGGGCGCGCTGGCAGAAACCGAGCGGAGCTGCAACCAACCGG 862
 Db 828 CTTGCTCAACCGCTGTGGCGGAGGCTGGCAGAAAGCGCACCGACCTGCACCAACCCCG 887
 Qy 863 CGCCTCTCAACGGGGGCGCTTCTGTGAGGGGCGAGATGTCAGAAACAGACCTGCGGCCA 922
 Db 888 CTCACACTCAACGGAGGGGCGCTTCTGCGAGGGGCGAGGCAATTCAGAAAGCGCGCTGCACCA 947
 Qy 923 CCTGTGCGCCAGTAGACGGGAGCTGGAGCGCGCTGGAGCAAGTGTGCGGCTGTGGGCTGG 982
 Db 948 CCATGCGCCAGTGCATGGGGCGTGGAGGAGTGGAGGAGTGGTGCAGCTTGCAGCACTG 1007
 Qy 983 ACTGCAACCACTGCGGAGCGGTGAGTGTCTGACCCAGCAACCCCGCAAGCGAGGGAGG 1042
 Db 1008 AGTGTGCCCACTGGCGTAGCGCGAGTGCATGGCGGCCCGCACCCAGAAAGCGAGCGCGTG 1067
 Qy 1043 AGTGCAGGACACTGACTGAGACCCGCACTGTACAGTGAACCTCTGTGTACACAGTG 1102
 Db 1068 ACTGACGGGAGCGCTGCTGCACTTAAGAACTGCACAGATGGGCTGTGTGATGCAACTGG 1127
 Qy 1103 CTTCTGCGCCCTGAGGACGTGGCCCTCTATGTGGGCTCTATCGCGCGTGGCGCTGCGCTGG 1162
 Db 1128 AGGCTCAGGGGATGCGCGCTGTATGGGGGCTGTGGTGGCCATCTTGTGTGTCTGG 1187
 Qy 1163 TCTGTGCTGTGTCTCTATCTCTGTTTATTCGCGGAAGAGAGGGGCTGGACTCAG 1222
 Db 1188 CAATCCTCATGGCGTGGGGGTGGTGTACCGCGCMACTGCGCGTGAATTCGACACAG 1247
 Qy 1223 ATGTGGCTGACTCTCTCAATT---CTCACCTCAGGCTTCCAGCCGCTCAGCATCAGGCCCA 1279
 Db 1248 ACATCACTGACTCATCTGCTGCGCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG 1307
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 Db 1308 CAAGGCCAGTAACCCGAGCTCTTACACCCCTGTGTGCTCTGACTGACAGCCAGCG 1367
 Qy 1334 CCACCACTACAGGGGAGTCTGTGCTCCGCGCAGGA----- 1370
 Db 1368 CCGGCATCTACCGCGGACCGCTGTATGCTCTGCGAGGACTCCACCGCAAAAATCCCATGA 1427
 Qy 1371 -----TGGGCGCCAGCCCAAGTTCCAGTCACTACCA----- 1399
 Db 1428 CCAACTCTCTCTGCTGAGACCCCTTACCCAGCCTTAAGGTCAGGTTACAGCTCCAGCA 1487
 Qy 1400 ---ATGGGCACCTGCTCAGCCCGCTGGGTGGCGGCGCGCACAC-----ACTGCACC 1447
 Db 1488 CCACGGGCTCTGGGCGCAGGCTGCGAGATGGGGCTGACCTGCTGGGGGTCTTGGCGCTG 1547
 Qy 1448 ACAGCTCTCCCACTCTGAGCGGAGGAGTTCGTTCTCCGCGCTCTCCACCCAGAACTCACT 1507

Db 1548 GCACATACCTAGCGATTTTCGCCGGGACACCCACTTCTCTGACCTTCGCGAGCGCCAGCC 1607
 Qy 1508 TCCGCTC-----CCTGCCCGAGGCCACAGCAACATGACCTATATGGACCT 1552
 Db 1608 TCGGTTCCAGAGAGCTCTTGGGCGTGCCTCCGAGACCAGGGAGCAGCGTCAGCGGACCT 1667
 Qy 1553 TCAACTTCTCTGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCTCATTCCTCC 1612
 Db 1668 TTGGCTGCTGGGTGGGAGGCTCAGCATCCCGGCAAGAGGGTCTGTGTGTGCCCCA 1727
 Qy 1613 CAGATGCATACCCCGAGGGAAGATCTATGAGATCTACCTCAAGCTCAAGCCGGAAG 1672
 Db 1728 ATGAGGCATTCGCCAGGCAAGTTCTACGAGATGTATCTACTCATCAAGGAGAGAA 1787
 Qy 1673 ACGTGAGTTGCCCTAGCTGCTGTCAGACCCCTGCTGAGTCCCATGTTAGCTGTGGAC 1732
 Db 1788 GTACCTTGGCGCTTTCAGAAAGGGACCCAGACAGTATTGAGCCCTCTCGGTGACCTGTGGAC 1847
 Qy 1733 CCGCTGCGCTCTGCTCACCGCGCCAGTCACTCTGGCTATGGACCACTGTGGGAGGCCCA 1792
 Db 1848 CCAGAGGCTCTGCTGTGCGCGCCCTCATCTCACCATGCCCACTGTGCGGAGTCA 1907
 Qy 1793 GCCTTGACAGCTGAGGCTGCGCTCAAAAAGCAGTCTGCGAGGCGAGCTGGGAGAGTG 1852
 Db 1908 GTGCCGTGACTGGATCTTTTTCAGCTCAAGACCCAGGCGCCACAGGGGCACTGGGAGAGG 1967
 Qy 1853 TGCTGACCTGGGCGAGGCGCCCTCCACCTCTACTCTACTGCGACGTGGAGGCCAGTG 1912
 Db 1968 TGGTGAACCTGGATGAGGAGACCTGAAACACACCCCTGCTACTGCGACGTGGAGCCAGGG 2027
 Qy 1913 CTTGCTACGCTTTCACCGAGCAGCTGGGCGCGCTTGGCTTGGTGGGAGAGGCCCTCAGCG 1972
 Db 2028 CTTGTACATCTCTGCTGGACAGCTGGGCACTACGTGTTCACGGGCGAGTCTCTATTTCCC 2087
 Qy 1973 TGGTGCCTGCGCAAGCGCTCAAGCTGTCTTGTGTGGCGCGGTGGCTGCACTCTCCCTG 2032
 Db 2088 GCTCAGCAGTCAAGCGGCTCCAGCTGGCGCTTTCGCGCCCGCCTCTGCACTCTCCCTGG 2147
 Qy 2033 AGTACACATCCGGGTCTACTGCTGATGACACCCAGCATGCACTCAAGGAGGTGTGC 2092
 Db 2148 AGTACAGCTTCCGGGTCTACTGCTGGAGGACAGCGCTGTAGCACTGAAGAGGTGTGG 2207
 Qy 2093 AGTGGAGAGAGCAGCTGGGCGGACAGCTGATCCAGGAGCCACGGGTCTCTGCACTTCAAGG 2152
 Db 2208 AGCTGGAGCGGACTCTGGGCGGATCTTGTGTGGAGGAGCCGAAACCGCTATGTTCAGG 2267
 Qy 2153 ACAGTTACCAACACTGCGCTATTCATCCAGATGTGCCAGCTCTCTGTGGAAGATA 2212
 Db 2268 ACAGTTACCAACACTGCGCTCTCTCTCCATGACCTCTCCCATTTGGAGGAGCA 2327
 Qy 2213 AGCTCTTGTGCTAGCTACCGAGGATCCCTTTTATCAGATCTGGAAATGGCAGCGCGGT 2272
 Db 2328 AGCTGTGGGCAAAATACAGAGATCCCTCTTCTATCACTTTGGAGTGGCAGCGCAAGG 2387
 Qy 2273 ACTTGCACTGCACTTTCACCTTGGAGCGTCTGAGCCCGCAGCACTAGTGAAGCTGGCTTGA 2332
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 Db 2448 AGATCTGCTGCGGCAAGTGGAAAGGGGAGGGCCAGATATTCAGAGTGCATACCACTCTGG 2507
 Qy 2393 CCAAG--GACACAGGTTTGTGCTGTGCTCTGAGAGTGAAGCGGGGTCCAG 2449
 Db 2508 CAGAGACACCTGTGTGGCTTCCCTGGACACTCTCTGTCTTGCCTTGGCAGCACTGTCA 2567
 Qy 2450 CCCTGTGGGCGCCAGTGCCTTCAAGATCCCTTCTCTTCTATTCGGCAGAAATATTTCCA 2509
 Db 2568 CCAGCTGGGACCTTATGCTTCAAGATCCCATGTCTCCATCCCGCAGAAATATGCAACA 2627
 Qy 2510 GCTTGAGACCACTCTGTAGGCGGGGTGCGAGTGTGGGAGCTCTGGGCCAGAACTCCACC 2569
 Db 2628 GCCTAGATGCCCCCAACTCACGGGCGAAATGACTGGCGGATGTTAGCACAGAACTCTCTA 2687

Qy	2570	TGGACAGCCATCTCAGCTTCTTTGGCTCGAAGCCAGCCCCACAGCCATGATCCTCAACC	2629
Db	2688	TGGACCGGTACCTGAATTACTTTGGCCACCAAGCGAGCCCGGGTGTGATCCTGGACC	2747
Qy	2630	TGTGGGAGGCGGCGCACTTCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTG	2689
Db	2748	TCTGGGAAGCTCTGCAGCAGGACGATGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGG	2807
Qy	2690	GACTGGGCCAGCCAGACGCTGGCCCTTTACAGTGTGCGAGGCTGAGTGTGA	2742
Db	2808	AGATGGGCAAGAGTGAGATGCTGTGGCTGTGGCCACCGACGGGACTGCTGA	2860

Search completed: August 8, 2005, 04:37:52
 Job time : 2468 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 11:56:52 ; Search time 13388 Seconds
(without alignment)
7824.385 Million cell updates/sec

Title: US-10-624-932C-1

Perfect score: 2752

Sequence: 1 ccgcggggcccccgcgcgg.....tgagtgctgagcggccag 2752

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_btc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	960.2	34.9	2802	9 AY406491	AY406491 Homo sapi
2	950.4	34.5	2791	9 AY406493	AY406493 Mus muscu
3	923.4	33.6	3790	3 AK031655	AK031655 Mus muscu
4	884	32.1	1852	3 CR598115	CR598115 full-leng
5	872.4	31.7	3866	3 AK018177	AK018177 Mus muscu
6	814	29.6	2802	9 AY406492	AY406492 Pan trogl
7	810.4	29.4	2532	9 AY411747	AY411747 Homo sapi
8	780.4	28.4	2532	9 AY411749	AY411749 Mus muscu
9	768.6	27.9	1034	4 B1758231	B1758231 603029876
10	736.6	26.8	1532	3 BC033727	BC033727 Homo sapi
11	735.2	26.7	788	1 A1951556	A1951556 wv36f04.x
12	721.6	26.2	796	5 BX348193	BX348193 BX348193
13	716.4	26.0	818	4 B1818609	B1818609 603033362
14	692	25.1	853	5 BX364574	BX364574 BX364574
15	678.2	24.6	2532	9 AY411748	AY411748 Pan trogl
16	672.6	24.4	934	2 BF311804	BF311804 601897316
17	666	24.2	900	5 BX345406	BX345406 BX345406
18	665	24.2	859	2 BF311896	BF311896 601897733
19	645.2	23.4	977	5 BX345407	BX345407 BX345407
20	631.2	22.9	1072	5 BX422753	BX422753 BX422753
21	618.8	22.5	756	5 B0612387	B0612387 UI-M-EWO-
22	613.2	22.3	874	5 B0689148	B0689148 AGENCOURT
23	610.2	22.2	2775	9 AY401471	AY401471 Mus muscu
24	607	22.1	889	5 B0691915	B0691915 AGENCOURT

25	599	21.8	2775	9 AY401469	AY401469 Homo sapi
26	595.2	21.6	601	1 AL516580	AL516580 AL516580
27	589.4	21.4	604	2 BE314370	BE314370 601147261
28	586.6	20.6	678	6 CA749784	CA749784 UI-M-FDO-
29	561	20.4	1175	2 BF530640	BF530640 602071931
30	555.6	20.2	788	6 CA317532	CA317532 UI-M-FWO-
31	555	20.2	572	7 CR554569	CR554569 DKF2p4591
32	494.2	18.0	499	7 CR747398	CR747398 CR747398
33	486.2	17.7	548	5 BX452510	BX452510 BX452510
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35	471.2	17.1	540	4 B1467799	B1467799 389583 MA
36	470.8	17.1	2507	9 AY401470	AY401470 Pan trogl
37	438.2	15.9	675	6 CA315487	CA315487 UI-M-FWO-
38	433	15.7	471	5 BX282095	BX282095 BX282095
39	428.4	15.6	1147	5 B0840446	B0840446 AGENCOURT
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41	417.8	15.2	856	7 CN164143	CN164143 994266 MA
42	411.8	15.0	749	7 CF735417	CF735417 UI-M-HB0-
43	410.6	14.9	1111	4 BG298307	BG298307 602397080
44	409.8	14.9	751	7 CF735550	CF735550 UI-M-HB0-
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ALIGNMENTS

RESULT 1	AY406491	2802 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY406491	Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,			
DEFINITION	AY406491	genomic survey sequence.			
ACCESSION	AY406491	GI:39762465			
VERSION	AY406491.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2802)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Infering nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2802)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment				
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gene	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
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	/locus_tag="HCM2575"				
ORIGIN					
Query Match	34.9%	Score	960.2	DB 9	Length 2802
Best Local Similarity	61.3%	Pred. No.	6.4e-192		
Matches 1682	Conservative	0	Mismatches 995	Indels 69	Gaps 6
QY	57	GC	CGCGCCTGTGCCACGCTCCTCGGCATAGTCCTCGCGCTTGGCTCGCGCTCGG	116	

Qy 1103 CTCTGSCCTGAGGAGCTGGCCCTCTATGTGG---CCTCATCGCGTGGCGTCTGCC 1159
Db 1107 CTCTGACTCAGATGATGTGGCTCTCTACGTGGGATTTGATCGCTGTAAACAGTCTGTC 1166
Qy 1160 TGGTCTGCTGCTGCTCTCATCTCCCTGTTATTGTCGGAAGAGGAGGGGCTGACT 1219
Db 1167 TGGGATCACTGTTGTGTGGCCCTGTTGTGTATCGAAGAACCCAGTGTGACTTTGAGT 1226
Qy 1220 CAGATGGGTGACTCGTGCATTTCTACCTCAGGCTTCCAGCCGTCAGCATCAAGCCCA 1279
Db 1227 CTGACATCAATGACTCTCTCAGCACTCAATGGCGGCTTTACGCTGTGAACATCAAG--- 1282
Qy 1280 GCAAAGCAGCAACCCCATCTGTCTACCATCCAGCGGACCTCAGCACCAACACACCA 1339
Db 1283 -----GCTGCCAGACAAGATCTCTGGCTGTCCCCCTGACCTCACCTCAGCTGCA 1337
Qy 1340 CCTACCAAGGAGCTCTCTGTCGCCCGGAGGATG-----GGCCAGACGCCCAAGTTCAGCT 1394
Db 1338 TGTACAGGGACCTGCTCTATGCTCTGATGATGTCTCAGACAAAATCCCAATGACCACT 1397
Qy 1395 CACAAATGGGCACTGCTCAGCCCCCTGGTGGGCGGCCCAACAACACTGCACACAGCTC 1454
Db 1398 CTCCAATTTCTGGACCCCACTACCCAACTTGAATAATCAAAAGTGTACAACAGCTCAGGTGCTG 1457
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Db 1578 CATCTGCACAGCATTTGGTACCTTCAACTCTCTGGGGGTCACTCATCATTTCTTAAT 1637
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Qy 1649 ACCTCAGCTGCACAAGCCGGAAGAGTGTGTGAGTTGCCCCCTAGCTGGCTGTGAGACCTCTG 1708
Db 1698 ATGTGACTGTACACAGGAAGAAATATAGGCCCCCACTGGAAGACTCTCAGACCCCTAC 1757
Qy 1709 TGAGTCCCATCGTTAGCTGTGACCCCTCGCTGGCTGTCTGCTCAACCGGCCAGTCACTCTGG 1768
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Qy 1889 ACTACTGCCAGCTGTGGAGCCAGTGTCTGTACGTCTTTCACGAGCAGCTGGGCGGTTTG 1948
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Qy 1949 CCCTGGTGGAGAGGCCCTCAGAGTGGCTGCGCCGAAGCCCTCAAGCTGCTCTCTTTG 2008
Db 1998 CCCTGGTGGGAGTCCACCACCAAGCACTGCCAAGCGCTTAACTGGCCATCTTTG 2057
Qy 2009 CGCGGTGGCTGCACCTCCCTCGAGTACAACTCCGGGTCTACTGTGCTCATGACACCC 2068
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Qy 2069 ACATGACACTCAAGAGGTGTGAGCTGTGAGAGAGAGCTGGGGGAGACAGCTGATCAGG 2128
Db 2118 AGGATGCCCTGAAGGAAGTTCTCAACTGGAGAGGCAAAATGGGAGGACAGCTCTCTAGAAG 2177
Qy 2129 AGCCACGGGTCTTGCACTTCAAGGACAGATTTACCACAACCTGCGCCTATCCATCCAGATG 2188

Db 2178 AACCCAGGCTCTTCATTTTAAAGGAGAGCATCCACAACCTTGCCTGTCTATTATGACA 2237
Qy 2189 TGCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTGAGCTACCAAGAGATCCCTTTTATC 2248
Db 2238 TGCCCATTTCCCTCTGGAAGAGCAAAATGCTGCTAAGTATCAGGAAATTTCCATTTTACC 2297
Qy 2249 ACATCTGGAATGGAACGCAAGCGGTAATTGCACTGTGACCTTTCACCTGGAGCGTGTACGC 2308
Db 2298 ACATCTGGAGTGGCTCTCAAGAAACCTCCACTGCACCTTCACTCTGGAAGAGACTCAGCC 2357
Qy 2309 CAGCACTAGTGAACCTGCAAGCTGTGGTGTGGCAGGTGGAGGGCGAGGGCGAGA 2368
Db 2358 TAAACACAGTGAACCTGGTTTGCAAACTCTGTGTGGCGAGGTTGAAGGAGAAAGGCGAGA 2417
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Db 2658 CAACTGGCGTAATCTCTGATCTTTGGGAAGCACAAGAACTTCCAGATGGAACCTGAGCA 2717
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Qy 2729 AGGCTGAGTCTGA 2742
Db 2778 AAGGACAGTATTGA 2791

RESULT 3
AK031655
LOCUS
DEFINITION
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030473H24 product:unc5 homolog (C.
elegans) 3, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK031655
AK031655.1 GI:26327502
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Kono, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Murakami, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

REFERENCE

4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

REFERENCE

5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

REFERENCE

6 Nature 420, 563-573 (2002)

REFERENCE

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tonaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

REFERENCE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

Location/Qualifiers

FEATURES

source

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/mol_type="mRNA"
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CD5

CD5

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ORIGIN

Query Match 33.6%; Score 923.4; DB 3; Length 3790;
Best Local Similarity 61.3%; Pred. No. 3.9e-184;
Matches 1659; Conservative 0; Mismatches 926; Indels 120; Gaps 6;
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455 AAACCTCTGGTCTAAATTTGAGAGAAGTGAAGATTGAGATTTTACGCCGAGGAGTGGAG 514
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995 TCAATGGTGGGCGCTTCTGTGAGGGGCGAGTGTGCAGAAAATAGCATGCACACTAT 1054
929 GCCCAGTAGACGCGAGCTGGAGCCCGCTGGAGCAAGTGGTGGGCTGTGGGCTGCACTGCA 988

[illegible][illegible]

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue

REFERENCE 2 (bases 1 to 1852)
AUTHORS Genoscope.
JOURNAL Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES Location/Qualifiers
source
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/db_xref="taxon:9606"
/clone="CS0DA006YG16"
/tissue_type="Neuroblastoma"
/plasmid="pCMVSPORT_6"

ORIGIN

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Matches 884; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGAGCGCCCTCCACCTTACTACTGCGAGCCAGGCGGCTGCTACGCTTTTCAC 60
Qy 1929 CGACAGCTGGCGCGCTTTGCCCTGTGGAGAGGCCCTCAGCTGGTGGCCGCAAGCG 1988
Db 61 CGACAGCTGGCGCGCTTTGCCCTGTGGAGAGGCCCTCAGCTGGTGGCCGCAAGCG 120
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Db 121 CCTCAAGCTGCTTCTGTTGGCGCGGTGGCTGCACCTCCCTCCAGTACACATCCCGGT 180
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Db 301 GCGCTATCCATCCACGATGCGCCAGCTCCCTGTGGAAGAGTAAGCTCTTGTGAGCTA 360
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Db 361 CCAGGAGATCCCCCTTTTATCACTCTGGAATGGCAGCGGCTTGTGCACTGCACCTT 420
Qy 2289 CACCTGAGGCTGTACGCCACGACATAGTACCTGGCTGCAAGCTGTGGGTGTGGCA 2348
Db 421 CACCTGAGGCTGTACGCCACGACATAGTACCTGGCTGCAAGCTGTGGGTGTGGCA 480
Qy 2349 GGTGGAGGGGACGGGCGAGAGCTTCAGCATCACTCAACATCAACGAGNCAAGGTT 2408
Db 481 GGTGGAGGGGACGGGCGAGAGCTTCAGCATCACTCAACATCAACGAGNCAAGGTT 540
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Db 841 TGGCTCTTCCACAGTTCGAGGCGTGTGCTGAGGCGCGGCGCAG 884
RESULT 5
AK018177
LOCUS
DEFINITION Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
enriched library, clone:6330415B02 product:TRANSMEMBRANE RECEPTOR
UNC5H2 homolog [Rattus norvegicus], full insert sequence.
ACCESSION AK018177
VERSION AK018177.1 GI:12857775
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
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Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636
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prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20493174
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Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
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Genome Res. 10 (11), 1757-1771 (2000)
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The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
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Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,

1560	GTGCCCGCTTTTGTGGTGGTATAGCGGTTCTCATGGCCGAGGAGTGATCGTATATACCGAGA	1619
1201	AAGAAGAGGAGGGCTTGGACTCAGATGTGGCTGACTCGT---CCAATTCTCACCTCAGGCTTC	1257
1620	AATCGCGGAGTTCGACACGGACATCACCGACTCTCTCTGGGCGCTTCACTGGTGGCTTC	1679
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1312	CAGCGGACCTCAGCACACACACACCTTACCAGGCGAGTCTCTGTCTCCCGCAGGA-	1370
1740	CCTCCAGACCTTAACGGCGAGTGGCATCTTACCAGCGGCGCTGTGTATGTCCTTCAGGAC	1799
1371	-----TGCGGCCGAGCCCAAG	1386
1800	TCCGCCCAAGATCCCACATGACTAATTGCCCTCTGTGGATCCCCGTGCCGAGCTCAAG	1859
1387	TTCAGCTCACCANTGGGCACTGCTCAG-----C	1416
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1920	CTGTGGGTGTCTCCCGCGGGCACGTAACCCAGCGAATTTCTCCCGGACACCCATTTC	1979
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2071	GATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGACAGCTGATCCAGGAG	2130
2580	GTAGCATGAAGGAGGCTCTGGAGCTGGAGGAGTCTTGGGTGGCTACTTGGTGGAGGAG	2639
2131	CCAAGGCTCTGCATTTCAAGGACAGTTTACCAAACTGCGCCTTATCCATTCACGATGTG	2190

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Qy	2311	AGCACTAGTGCACCTGGCCTCCAAAGCTGTGGTGTGGCAGGTGGAGGCGACGGSCAGAGC	2370
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Db	2880	TTCCAGCTGCACACAACGTTTGGCCGAGACGCCCTGCTGGCTCCCTGGATGCTCTCTGCTCT	2939
Qy	2428	GAGAGTGAAGCGGGGTCCCAAGCCCTGGTGGGCGCCAGTGCCTTCAAGATCCCTTCTCTC	2487
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Qy	2548	ACTCTGCCCGAGAACTTCACTGGACAGCCATCTCAAGTCTTTTGTCTCAAGCCGACG	2607
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Qy	2668	CAGCTGCTGCAGCAGTGGCTGGACTGGGCGACGACGCTGGCCTCTTTCACAGTGTG	2727
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Db	3240	GATGGCGATTGCTGAG	3255

RESULT 6	AY406492	2802 bp	DNA	linear	GSS 15-DEC-2003			
LOCUS	AY406492	Pan troglodytes UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.						
DEFINITION	AY406492							
ACCESSION	AY406492							
VERSION	AY406492.1	GI:39762466						
KEYWORDS	GSS.							
SOURCE	Pan troglodytes (chimpanzee)							
ORGANISM	Pan troglodytes							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.							
AUTHORS	1 (bases 1 to 2802)							
	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.							
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios							
JOURNAL	Science 302 (5652), 1960-1963 (2003)							
PUBMED	14671302							
REFERENCE	2 (bases 1 to 2802)							
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.							
TITLE	Direct Submission							
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA							
COMMENT	This sequence was made by sequencing genomic exons and ordering							

FEATURES		them based on alignment.		Location/Qualifiers	
source		1. .2802		/organism="Pan troglodytes"	
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gene		<1. -2802		/gene="UNC5C"	
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ORIGIN					
Query Match 29.6%; Score 814; DB 9; Length 2802;					
Best Local Similarity 53.8%; Pred. No. 4.7e-161;					
Matches 1477; Conservative 0; Mismatches 1200; Indels 69; Gaps 6;					
Qy	57	GCCTGGCTGTGGCCAGCGCTCTGGGCATAGTCTCGCGCTTGGCTCGCGCTCGGG	116		
Db	66	GCTGTGCTACCTGTGCCCTGCTCAGCGCAGCGCACCTGGCTCCGCGCCCAAGA	125		
Qy	117	TGCCCAGCAGTGCACACCTGGCCAAACCCAGTGCCTGTGTGCCAACCCGGACCTGTTC	176		
Db	126	TGATGACTTTTTCATGAACCTCCAGAAACTTTTCTTGGATCCACCTGAGCCTCTGCC	185		
Qy	177	CCACTTCTGTGTGAGCCGAGATGTATCATGCTCAAGAAACAAGCAGTGTCTGTGT	236		
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Db	366	NN	425		
Qy	411	CTGGTGCCAGTGGTGCATGGAGCTCTCGGGCAACCAAGAGTCAAGAGCCCTACAT	470		
Db	426	NN	485		
Qy	471	CCGCATAGCCAGATTGGCAAGAACTTCGAGCAGGAGCCCTGGCCAAAGAGTGTCCCT	530		
Db	486	NN	545		
Qy	531	GGAGCAGGCACTGTGTGCTGCTGCCCTCCACCGGAGGCGATCCCTCCAGCCGAGGTGA	590		
Db	546	GGACAGGAAGTCTTACTCCAGTGTGGCCACCTGAAGGATCCAGTGGCTGAGNNNN	605		
Qy	591	GTGGCTCCGGAACAGAGAACCTGTGTGAACCGTCCCTGGACCCCAATGTATACATCAGCG	650		
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Qy	651	GGAGCAGCCTGTGTGTGCGACGAGCCGCTGTGTGACACGGCCAACTACACCTGCGT	710		
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RESULT 7
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LOCUS 2532 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION AY411747
VERSION AY411747.1 GI:39767715
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2532)
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source 1..2532
/organism="Homo sapiens"
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Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 2532)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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Query Match 29.4%; Score 810.4; DB 9; Length 2532;
Best Local Similarity 61.1%; Pred. No. 2.7e-160;
Matches 1540; Conservative 0; Mismatches 851; Indels 129; Gaps 9;

Qy 352 GAGTTCGCGATTATGTCTCAAGCGCAGCGTTCGAGAAGGTGTTTCGGGCTGGAGGAATAC 411
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Qy 472 CGCATAGCCAGATTGGCAAGAACTTCGACAGAGAGCGCTGGCCAGAGAGGTGTCCCTG 531
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Qy 532 GAGCAGGGCATCTGTCTGCCCTCGCTGCACCGAGGGCATCCCTCCAGCGAGGTGGAG 591
Db 193 GACCATGAGGTTCTCTGCGAGTCCGCCCGCGGAGGGGTGCTGTGGCGAGGTGGAA 252
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Qy 1012 TCTGACCCAGCACCCCGCAACGAGGGGAGTGGCAGGGCACTGACCTGGAGACCCCGC 1071
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QY 2503 ATTTCAGCTGTGAACCCACCTGTAGGCGGGTGGCGACTGGCGGACTCTGGCCCGAGAA 2562
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RESULT 8
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LOCUS Mus musculus HCM4327 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY411749
VERSION AY411749.1 GI:39767717
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2532)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2532)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
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TITLE      Adams,M.D. and Cargill,M.
JOURNAL    Direct Submission
COMMENT    Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
           Rockville, MD 20850, USA
           This sequence was made by sequencing genomic exons and ordering
           them based on alignment.
FEATURES   Location/Qualifiers
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                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:10090"
            gene            <1..>2532
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Query Match	28.4%; Score 780.4; DB 9; Length 2532;
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Matches 1515; Conservative 0; Mismatches 876; Indels 129; Gaps 8;	
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QY	412 TGGTGCACAGTCGTGGCATGAGCTCTCGGGCACCAACCAAGAGTCAGAAAGCCCTACATC 471
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QY	73 TGGTGCACAGTCGTGGCTGGAGCTCTTCGGGAACCTACCAAGAGTCGCCGAGCCCTACATC 132
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QY	472 CGCATAGCCAGATTGCGCAAGAACTTCGAGCAGAGCGCGCTGGCCAAAGGAGTGTCCCTG 531
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QY	133 CGCATTCGCTACTTTCGCAAGAACTTTTGACAGAGGCTCTGGCCAAAGGAGTACCCCTG 193
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QY	193 GATCATGAGGTCCCTTCGTGCAAGTCGCGCCACCGAGGAGGTGCCTGTGGCTGAGGTGGAA 252
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QY	313 GACCACAACTCATCATCCGCGAGCGCGCTCTCAGACACGGCCAACTACACCTGTGTG 372
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QY	712 GCCAAGAACATCGTGGCACGTCGCGCGAGCGCCCTCGCTGCTGTCATCGTCAAGTCAAC 771
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QY	373 GCCAAGAAATTCGTGGCAAGCGCCGAGACACACGGCCACAGTCATCGTCTATGTGAAT 432
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QY	772 GGTGGGTGGTCGAGTGGACCGAGTGGTTCGCTCTGCAGCGCCAGCTGTGGGCGCGGTGG 831
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QY	433 GGAGGCTGGTCCAGCTGGGCGAGTGTGTCAACCTGTTCCAATCGCTGTGGCCGAGGCTGG 492
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QY	673 ATGGCACCGGCACCCCAAGAACGGAGGCGGTGACTGCGAGCGGGACGCTACTTGACTCCAAG 732
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Qy	1273	AAGCCAGCAAGCAGACACACCCCATCTGCT-----CACCATCCAGCCGACCTCAGC	1326
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Qy	1966	CTCAGCGTGGCTGCCCGCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCCTGCACC	2025
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Db	1813	TCCCTGGAGTATAGCTCTCAGGGTCTACTGTCTGGAGACACACTGTAGCACTGAAGGAG	1872
Qy	2086	GTGGTCAAGCTGGAGAACAGCTGGGGGACAGCTGATCCAGGAGCCACGGTCTCTGCACT	2145
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Db	777	GTGCCAGTGGACGCGCAGCTGTAGACAGCTGTGGAGCCAGTGTGCGGCTGTGGGCTTTGGCTT	836
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RESULT 10	BC033727	LOCUS	BC033727	1532 bp	mRNA	linear	HTC 25-MAR-2004
DEFINITION	Homo sapiens unc-5 homolog A (C. elegans), mRNA (cDNA clone IMAGE:5166762), containing frame-shift errors.						

SOURCE
ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 796)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 5, 2003 this sequence version replaced gi:30367258.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3239.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0BAF0042D01_AF00293_1&c=3239.r

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 /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 Query Match 26.2%; Score 721.6; DB 5; Length 796;
 Best Local Similarity 96.4%; Pred. No. 1.3e-141;
 Matches 758; Conservative 0; Mismatches 26; Indels 2; Gaps 2;

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 2098 GAGAAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGTCTGCTCAAGGACAGT 2157
 2158 TACCACAAACCTGGCGCTATCCATCCACGATGTGCCAGCTCCCTGTGGAGAGTAAGCTC 2217

SOURCE
 316 TACCACAAACCTGGCGCTCATCATCCAGATGTGCCAGCTCCCTGTGGAGAGTAAGCTC 257
 2218 CTTGTGAGCTACAGAGATGCCCTTTTATCATCTGGAATGCGACGCGGTACTTG 2277
 256 CTTGTGAGCTACAGAGATGCCCTTTTATCATCTGGAATGCGACGCGGTACTTG 197
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 2458 GGCCCC 2463
 16 GGCCCC 11

RESULT 13
LOCUS BI818609
DEFINITION 60303362F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174559 5', mRNA sequence.
ACCESSION BI818609
VERSION BI818609.1 GI:15929902
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 818)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Cloning Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLML1434 row: 1 column: 16
 High quality sequence stop: 744.
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 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

FEATURES
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ORIGIN
 Query Match 26.0%; Score 716.4; DB 4; Length 818;
 Best Local Similarity 97.7%; Pred. No. 1.7e-140;

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Db	61	CTCCGGGCTCGGCTGGTGGCCACGACAGATGCCACCGTGGCCAAACCAGTGCCTGTGTGCCAAC	120						
Qy	163	CCGGACCTGTTTCCCACTTCTCGTGGAGCCCGCAGGATGTATACATCGTCAAGAAACAAG	222						
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Qy	223	CCAGTGTCTGTGTGTCAAGGCCGTGCCCGGCCACGCAGATCTTTCTTCAAGTGCACCGGG	282						
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Qy	283	GAGTGGGTGGCCAGGTGGACCACTGATCGAGCGCAGCAGACGAGCGGAGCAGTGGGCTG	342						
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Qy	343	CCACCATGAGGTCCGCAATTAATGTTCTCAAGGCAGCAGGTTCGAGAAAGTGTTCGGGCTG	402						
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Qy	403	GAGGAATATCTGGTGCAGTGGGTGGCATTGGAGTCTCTCGGSCACACCACAAAGTGCAGAA	462						
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Qy	463	GCCTACATCCGCATAGCCAGATTTCGCGCAAGAACTTCGACGACGAGCCGCTGGGCCAAGGAG	522						
Db	421	GCCTACATCCGCATAGCCAGATTTCGCGCAAGAACTTCGACGACGAGCCGCTGGGCCAAGGAG	480						
Qy	523	GTGTCCCTGGAGCAGGCGCATCGTCTGCCCTGCGGTCCACCGGAGGCGATCCCTTCAGACC	582						
Db	481	GTGTCCCTGGAGCAGGCGCATCGTCTGCCCTGCGGTCCACCGGAGGCGATCCCTTCAGACC	540						
Qy	583	GAGTGGAGTGGCTCCGGAACGAGGAACCTGGTGGACCCGTCCTTCGGAACCCCAATGTATAC	642						
Db	541	GAGTGGAGTGGCTCCGGAACGAGGAACCTGGTGGACCCGTCCTTCGGAACCCCAATGTATAC	600						
Qy	643	ATCACGGGGAGCACAGCCGTGGTGGGACAGGCCCGCCCTTGTGTGACAGGCCCAATCTAC	702						
Db	601	ATCACGGGGAGCACAGCCGTGGTGGGACAGGCCCGCCCTTGTGTGACAGGCCCAATCTAC	660						
Qy	703	ACCTGCGTGGCCAGAAACATCGTGGCACGTC - GCCGCGAGCGCCTCCGCTGCTGTCTATCGT	761						
Db	661	ACCTGCGTGGCCAGAAACATCGTGGCACGTCAGCCGCGAGGCCCTCCGCTGCTGTCTATCGT	720						
Qy	762	CTACGTGAAACGGTGGGTGGTCGACG - TGGACCGAGTGGTCGCTG	806						
Db	721	CTACGTGAAACGGTGGGTGGTCGACCGCGTTGGAGCCAGTGTGGGCTG	766						

RESULT 14
 BX364574
 LOCUS
 DEFINITION
 cDNA clone CS0DC023YB10 5'-PRIME, mRNA sequence.
 ACCESSION
 BX364574
 VERSION
 BX364574.2
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1. (bases 1 to 853)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 5, 2003 this sequence version replaced gi:30368812.
 COMMENT
 Contact: Genoscope

Qy 661 CTGGTGGTGGCAGAGCCCGCTTCTGACACGGCCAACTACACCTGGT 710
 Db 804 CTGGTGGTGGCAGAGCCCGCTTCTGACACGGCCAACTACACCTGGT 853

RESULT 15
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 DEFINITION Pan troglodytes HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY411748
 VERSION AY411748.1 GI:39767716
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 2532)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment.
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 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
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gene
 ORIGIN

Query Match 24.6%; Score 678.2; DB 9; Length 2532;
 Best Local Similarity 54.4%; Pred. No. 2.2e-132;
 Matches 1370; Conservative 0; Mismatches 1021; Indels 129; Gaps 9;

Qy 352 GAGTCCGCGATTAAATGTTCAAGCAGCAGGTTCGAGAGGTGTTTCGGGCTGGAGGAATAC 411
 Db 13 GAGTGCAGATCGAGGTGTCGCGCAGCAGGTGAGGAGCTTTTGGGCTGGAGATTAC 72

Qy 412 TGGTCCAGTCGTTGGATGAGTCTCTCGGGCAACACAGAGTCAAGAGCCCTACATC 471
 Db 73 TGGTCCAGTCGTTGGGCTGAGTCTCTCGGGCAACACAGAGTTCGCGAGCCTACGTC 132

Qy 472 CGCATGCCAGATTGCGCAAGAACTTCGACGAGGCGGCTGGCCAAGGAGGTTCCTCG 531
 Db 133 CGCATGCCCTNN 192

Qy 532 GAGCAGGCGCATCGTGTGCTGCGCTCCGTCACCGGAGGCGCATCCCTCCAGCGCGGTGGAG 591
 Db 193 NNN 252

Qy 592 TGGTCCGGAACGAGGACTGGTGGACCGGCTCTCGGACCCCAATGTATACATCACCGG 651
 Db 253 TGGCTCAAGATGAGGATGTATCGACCCCAACCCAGGACACCAACTTCTGCTCAACATC 312

Qy 652 GAGCACGCTGGTGGTGGCAGGCGGCTTCTGACACGGCAACTACCTGCGTG 711
 Db 313 GACCACAACTCATCCCGCAGGCGGCTGTCGACACATGCAATATACCTGCGTG 372

Qy 712 GCCAAGAACATCGTGGCAGCTGCGCGCAGCGCTCCGCTGCTGTGTCATCGTCTACGTGAAC 771
 Db 373 GCCAAGAACATCGTGGCAGCTGCGCGCAGCGCTCCGCTGCTGTGTCATCGTCTACGTGAAT 432

Qy 772 GGTGGGTGGTGCAGCTGGAACCGAGTGTCTGTGTCAGCGCCAGCTGTGTCGCGCGGTGG 831
 Db 433 GCGCGCTGGTCCAGCTGGGAGAGTGGTGGCCCTGCTCCAAACCGCTGTGGNNGANNCTGG 492

Qy 832 CAGAAAACGAGCGGAGCTGCACCAACCGCGGCTCTCAACGGGGGCGCTTCTGTGTGAG 891
 Db 493 CAGAAAGCGCACCCGAGCTGCACCAACCGCGGCTCTCAACGGAGGNNNNNTCTGCGAG 552

Qy 892 GGCAGAAATGTCCAGAAAACAGCCCTGCGCCACCCCTGTGTCAGCGAGCTGGAGC 951
 Db 553 GGCANNN 612

Qy 952 CCCTGGAGCAAGTGGTGGGCTGTGGGTGAGCTGCAACCCACTGGCGGAGCGGTGAGTGC 1011
 Db 613 GAGTGGAGCAAGTGGTGGGCTGTGAGCACTGAGTGTGCCACTGGCGGTAGCGCGAGTGC 672

Qy 1012 TCTGACCCAGCACCCCGCAACGAGGAGGAGTGCAGGGCACTGACCTCGACACCCCGC 1071
 Db 673 ATGGCGCCCCACCCAGAGAGCGGCGGTGACTGACGCGGAGCGTGTCTGACTCTAAG 732

Qy 1072 AACTGTACCAAGTACCTCTGTGTACACAGTCTTCT----- 1107
 Db 732 AACTGCACAGATGGCTGTGCATGCAAAATAAGAAACTCTAAGCGACCCCAACAGCCAC 792

Qy 1108 -----GGCCCTGAGAGCGTGGCCCTCTATGTGGGCTC---ATGCGCGTGGCGGTC 1155
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Qy 1156 TGCTGTGCTGCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1215
 Db 853 GTGNTGCAATTCCTATGCGGCGTGGGGTGGTGTGTACCGCCCAACTGCGGTGACTTC 912

Qy 1216 GACTCAGATGTGGCTGACTGCTCCATT---CTACCTCAGGCTTTCAGCGCGTCTGAGTTC 1272
 Db 913 GACACAGACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTCACCCCGTCACTTT 972

Qy 1273 AAGCCAGCAAGAGCAGCAACCCCTCATCTGCT-----CACCATTCAGCGCGGACTCAGC 1326
 Db 973 AAGACGGCAAGGCGCAGCAACCCGAGCTCTACACCCCTCTGTGCTCTCTGACTGACA 1032

Qy 1327 ACCACACACCACTTACAGGCGAGTCTCTGTCCTCCCGCGGAGGATGGG----- 1374
 Db 1033 GCCAGCGCGGCTCTTACCGCGGACCCGCTGTATGCTCTGAGGACTCCACGACAAATC 1092

Qy 1375 -----CCAGCGCCCAAGTTCAGCTCACCA-- 1399
 Db 1093 CCATGACCAACTCTCTCTGCTGGACCCCTTACCCAGCTTAAGGTCNAGGTCACAGC 1152

Qy 1400 -----ATGGGCACTCTCAGCCCTCTGGGTGGCGCGCGCC-----ACACA 1440
 Db 1153 TCCAGCACTACTCGGCTCTGGGCGAGGCTGGCAGATGGGCTGACCTGCTGGAGTCTTG 1212

Qy 1441 CTGCACCACAGCTCTCCACTCTGAGCGCAGAGTTCCTCCCGGCTCTCCACCGAG 1500
 Db 1213 CCCTCTGGCACATACCTTACGATTTTCGCGGAGACACCCACTTCTCTGCACTCTGCGAGC 1272

Qy 1501 AACTACTTCCGCTC-----CCTGCCCCGAGGCGACAGCAACATGACCTAT 1545
 Db 1273 GCCAGCTCGTTTCCAGCAGCTCTTGGGCTGCCCCGAGACCCAGNAGCAGGCTCAGC 1332

Qy 1546 GGGACCTTCAACTCTCTCGGGGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCT 1605
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Qy 1606 ATCCCCCAGATGCCATACCCCGAGGAGATCTATGAGATCTACTCAGCTGCAAG 1665
 Db 1393 GTGCCAAATGGAGCAATTCGCCAGGCGAAGTTCTAGAGATGTATCTACTCATCAACAG 1452

Qy 1666 CCGAAGACGTGAGGTGCGCTTAGCTGCTGAGTCCAGACCCCTGCTGAGTCCATCGTTAGC 1725

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Qy	41	AspLeuLeuProHisHisPheLeuValGluProGluAspValTyrIleValLysAenLysPro	60
Db	207	GACCTGCTTCCCACTTCTCGTGGAGCCGAGGATGTATCATCGTCAAGAAACAAGCCA	266
Qy	61	ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAenGlyGlu	80
Db	267	GTGCTGCTGTGTGCNAGCCGCTGCCCGCCACGCAGATCTTCTTCNAGTGCACGGGGAG	326
Qy	81	TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro	100
Db	327	TGGGTGGCCAGGTGGACACGTCATCAGCGCAGCACAGACGGGAGCAGTGGTGAGCCG	386
Qy	101	ThrMetGluValArgIleAenValSerArgGlnValGluLysValPheGlyLeuGlu	120
Db	387	ACCATGGAGGTCCGCAITTAATGTCTCAAGGCAGCAGGTGCGAAGAGGTGTTCGGGCTGGAG	446
Qy	121	GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla	140
Db	447	GAATACTGGTGCATGCGTGGCATGGAGTCTCTCGGGCACCAACAGAGTTCAGAGGCC	506
Qy	141	TyrIleArgIleAlaArgLeuArgLysAenPheGluGlnGluProLeuAlaLysGluVal	160
Db	507	TACATCGCATAGCAGATTCCGCAAGAACTTCGAGCAGGAGCGCTGGCCCAAGAGGTG	566
Qy	161	SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu	180
Db	567	TCCCTTGAGCAGGGGATGTGCTGCCCTGCCGTCCACGGAGGGCATCCCTCCACGCCGAG	626
Qy	181	ValGluTrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIle	200
Db	627	GTGAGTGGCTCCGGACGAGCACTGGTGGACCCGTCCTCGACCCCAATGATATCATC	686
Qy	201	ThrArgGluHisSerLeuValValArgGlnAlaArgIleAlaAspThrAlaAenTyrThr	220
Db	687	ACGCGGGAGCAGACCTGGTGGTCGACAGGCGCGCTTGTGTGACAGCGCCAACTACACC	746
Qy	221	CysValAlaLysAenIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr	240
Db	747	TGCTGTGCCAAGAACATCGTGGCAGTCGCCCGCAGCGCTCCGCTGCTGTCTCATCTAC	806
Qy	241	ValAenGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg	260
Db	807	GTGAAACGGTGGTGGTGACGTGACCGAGTGTCCGTCTGCACGGCCAGCTGTGGGCGC	866
Qy	261	GlyTrpGlnLysArgSerArgSerCysThrAenProAlaProLeuAenGlyGlyAlaPhe	280
Db	867	GGCTGGCAGAAACGGAGCCGAGCTGCACCAACCCGCGCTCTCAACGGGGCGCTTTC	926
Qy	281	CysGluGlyGlnAenVal----GlnLysThrAlaCysAlaThrLeuCysProValAspGly	299
Db	927	TGTGAGGGGCGAAGATGTCATAGACCGCACCGCTCTCTCTGCTGTGTCTCTGTGGACGGC	986
Qy	300	SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisLysTrpArgSer	319
Db	987	AGCTGGAGCCCGTGGAGCAAGTGTGGCCCTGTGGCTGTGGACTGCACCCACTGGCGGAGC	1046
Qy	320	ArgGluCysSerAspProAlaProArgAenGlyGlyGluGluCysGlnGlyThrAspLeu	339
Db	1047	CGTCAGTGTCTGTGACCCAGCACCCCGCAACGAGGGGAGGAGTGCACAGGCCTGACCTG	1106
Qy	340	AspThrArgAenCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal	359
Db	1107	GACACCCGCAACTGTATCAGATGACCTCTGTGTATACAGTGTCTTGTGGCCCTTGAGACGTG	1166
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Db	1167	GCCCTCTATGTGGGCCCTCATCGCCGTGGCCGTCTGCCCTGGTGTCTGCTGTGTCTCTC	1226
Qy	380	IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIle	399

1227	Db		ATCTCTGTTTATTGCGGGAAGAGGGGCGTGAGACTCAGATGTGGCTGACTCGTCCATT	1286
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1287	Db		CTCACTTCAGGCTTCAGAGCCGTCAGATCAAGCCAGCAAGAGCAGCAACCCCATCTG	1346
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1584	Db		TATGGGACCTTCAACTTCTCGGGGCGGCTGATGATCCCTAAATACAGGTATCAGCCTC	1643
520	Qy		LeuIleProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis	539
1644	Db		CTCATCCCCCAGATGCCATACCCGAGGAGAGATCTATGAGATCTTACCTCAGCTGCAC	1703
540	Qy		LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal	559
1704	Db		AAGCGGAGACGTGAGTTGCCCTAGCTGGCTGTACAGCCCTGCTGAGTCCCATCGTT	1763
560	Qy		SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys	579
1764	Db		AGCTGTGGACCCCTGGCGTCTGCTCACCGGCCAGTCACTCTGGCTATGGACCACGTG	1823
580	Qy		GlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySer	599
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600	Qy		TrpGlu---AspValLeuHisLeuGlyGluGluAlaProSerHisLeuTyxTyxCysGln	618
1884	Db		TGGGAGCAGATGTGTGTGACCTGGCGGAGGAGGCGCCCTCCACCTCTACTTACTGCCAG	1943
619	Qy		LeuGluAlaSerAlaCysTyxValPheThrGluGlnLeuGlyArgPheAlaLeuValGly	638
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639	Qy		GluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAla	658
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659	Qy		CysThrSerLeuGluTyxAsnIleArgValTyxCysLeuHisAspThrHisAspAlaLeu	678
2064	Db		TGCACCTCCCTCGAGTACAACTCCGGGTCTACTGCCTGCATGACACCCACCATGCACTC	2123
679	Qy		LysGluValValGlnLeuGlyGlnLeuGlyGlyGlnLeuIleGlnGluProArgVal	698
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RESULT 4

MMU487852
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 DEFINITION Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).
 ACCESSION AJ487852

VERSION AJ487852.1 GI:22035783

KEYWORDS netrin receptor Unc5h1; Unc5h1 gene.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Engelkamp,D.

Cloning of three mouse Unc5 genes and their expression patterns at

mid-gestation

Mech. Dev. 118 (1-2), 191-197 (2002)

22239710

12351186

2 (bases 1 to 3992)

Engelkamp,D.

Direct Submission

Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for

Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY

FEATURES

source

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ORIGIN

Alignment Scores:

Pred. No.: 3,59e-271 Length: 3992
 Score: 4685.00 Matches: 868
 Percent Similarity: 98.78% Conservative: 19
 Best Local Similarity: 96.66% Mismatches: 11
 Query Match: 97.79% Indels: 0
 DB: 10 Gaps: 0

US-10-624-932C-2 (1-898) x MMU487852 (1-3992)

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 Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
 Db 292 CGTGGTTTCGGGTGCCCGACGAGTGCCACAGTGGCCACCCAGTGCTGGTGCCAAACCCA 351
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 Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluIysValPheGlyLeuGlu 120
 Db 532 ACCATGGAGGTCCGATCAACGTATCAGGCGACGAGTGTGAGAAAGTGTGTGGGCTGGAG 591
 Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
 Db 592 GAGTACTGGTCCAGTGTGTGGCATGGAGTCTCTCAGGAACCCACCAAGAGGCC 651
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Qy 661 SerLeuLysTyrAenIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
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RESULT 5

CQ730306 2784 bp DNA linear PAT 03-FEB-2004
LOCUS Sequence 16240 from Patent WO02068579.
DEFINITION CQ730306
ACCESSION CQ730306.1 GI:42303801
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of human exons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 16240 06-SEP-2002;

PE Corporation (NY) (US)

Location/Qualifiers

source

1. .2784

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 5,28e-269 Length: 2784

Score: 4645.50 Matches: 881

Percent Similarity: 93.63% Conservative: 1

Best Local Similarity: 93.52% Mismatches: 1

Query Match: 96.96% Indels: 59

DB: 6 Gaps: 3

US-10-624-932C-2 (1-898) x CQ730306 (1-2784)

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QY 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
DB 61 CGGGCTCGGGTCCGCCAGCAGAGTGCCACCGTGGCCNACCAGTGCCTGGTGCACACCCG 120
QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
DB 121 GACCTGCTTCCCCACTTCTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGTCAACAGGCCA 180
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DB 181 GTGCTGCTGTGTGCAAGGCCGCTGCCCGCCACGACGATCTTCTCAAGTCAACAGGCCGAG 240
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QY 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
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QY 121 GluTyrTrpCysGlnCysValAlaTTPSerSerSerGlyThrThrLysSerGlnLysAla 140
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QY 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
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QY 352 -----SerAlaSerGlyPro 356
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Qy 617 CysGlnLeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeu 636
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RESULT 6
LOCUS AX268596
DEFINITION Sequence 15 from Patent WO0175440.
ACCESSION AX268596
VERSION AX268596.1 GI:16541710
KEYWORDS Rattus sp.

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ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and
Pratt,J.Y.
TITLE Schizophrenia related genes
JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;
WELFIDE CORPORATION (JP)
FEATURES
Location/Qualifiers
source 1..2697
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ORIGIN

Alignment Scores:
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Best Local Similarity: 95.99% Mismatches: 19
Query Match: 96.81% Indels: 0
DB: Gaps: 0

US-10-624-932C-2 (1-898) x AX268596 (1-2697)

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261	Qy	GlyTyrGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe	280
781	Db	GGCTGGCAGAAACGAGCGGAGCTGCACCAACCGCGCACCTCTCAACGGGGCGCCTTC	840
281	Qy	CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrIleuCysProValAspGlySer	300
841	Db	TGTGAGGGGCAAGATGTCAGAAACAGCCTGCGCCACTCTGTGTCCAGATGGATGGGAGC	900
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1321	Db	CAGGATGGACCCAGCCCAAGTTCAGCTCTCTAATGTCACCTGTCTCAGCCCACTGGG	1380
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RESULT 7	
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LOCUS	
DEFINITION	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds.
ACCESSION	U87305
VERSION	U87305.1 GI:2055391
KEYWORDS	
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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	Rattus.

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REFERENCE 1 (bases 1 to 2697)
AUTHORS Leonardo, E.D., Hincin, L., Masu, M., Keino-Masu, K., Ackerman, S.L. and Tessier-Lavigne, M.
TITLE Vertebrate homologues of C. elegans UNC-5 are candidate netrin receptors
JOURNAL Nature 386 (6627), 833-838 (1997)
MEDLINE 97271897
PUBMED 9126742
REFERENCE 2 (bases 1 to 2697)
AUTHORS Leonardo, E.D., Hincin, L., Masu, M., Keino-Masu, K. and Tessier-Lavigne, M.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA
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ACCESSION BD057524
VERSION 1 GI:22603130
KEYWORDS JP 2001505062-A/1.
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 3014)
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 1 17-APR-2001;
THE REGENTS OF THE UNIV OF CALIFORNIA
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PD 17-APR-2001
PF 19-FEB-1998 JP 1998536840
PR 19-FEB-1997 US 08/808982
PI MARC TESSIER LAVIGNE, DAVID E LEONARDO, LINDSAY HINCK, MASAYUKI
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LOCUS Sequence 13 from Patent WO0198354.
ACCESSION AX367094
VERSION AX367094.1 GI:118955296
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B.,
Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,
Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,
Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and
Sanjanwala,M.S.
TITLE Receptors
JOURNAL Patent: WO 0198354-A 13 27-DEC-2001;
INCYTE Genomics, Inc. (US)
FEATURES
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Best Local Similarity: 93.54% Mismatches: 1
Query Match: 92.11% Indels: 56
DB: 6 Gaps: 1

US-10-624-932C-2 (1-898) x AX367094 (1-3580)

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Qy      61  ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
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Qy      121  GluTyTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
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DEFINITION MGC:66671 IMAGE:6813463), complete cds.
ACCESSION BC058084
VERSION BC058084.1 GI:34784158
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 3844)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toehiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 3844)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Neess, Pawan Pandoh, Ana-Liisa Prabbu, Parvaneh Saedi, Jacqueline Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 136 Row: b Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

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Location/Qualifiers

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involved in cell death (apoptosis). Alpha-helical domain

present in a variety of proteins with apoptotic functions.

Some (but not all) of these domains form homotypic and

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ORIGIN

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Qy	641	LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThr	660
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Qy	661	SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu	680
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Qy	721	LyseSerLyseuLeuValSerTyGlnGluIleProPheTyHIsIleTyrAsnGlyThr	740
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DEFINITION		Mus musculus mRNA for mKTAAL1976 protein.	
ACCESSION		AKI22575	
VERSION		AKI22575.1 GI:28972881	
KEYWORDS		FLI CDNA.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS		Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S., Nakajima,D., Nagase,T., Ohara,O. and Koga,H.	
TITLE		Prediction of the coding sequences of mouse homologues of KIAA gene: II. the complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries	
JOURNAL		DNA Res. 10, 35-48 (2003)	
AUTHORS		2 (bases 1 to 4294)	
TITLE		Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.	
JOURNAL		Direct Submission	
AUTHORS		Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7	
TITLE		Kazusa-Kamatori, Kisarazu, Chiba 292-0818, Japan	
JOURNAL		(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)	
COMMENT		The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing: Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.	

FEATURES

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Alignment Scores:
Pred. No.: 1..476-176 Length: 4294
Score: 3107.00 Matches: 642
Percent Similarity: 49.77% Conservative: 13
Best Local Similarity: 48.78% Mismatches: 8
Query Match: 64.85% Indels: 654
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US-10-624-932C-2 (1-898) x AK122575 (1-4294)

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BC009333

LOCUS

DEFINITION Homo sapiens unc-5 homolog A (C. elegans), mRNA (cDNA clone IMAGE:4126760), partial cds.

ACCESSION BC009333

VERSION

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Strausberg, R.D., Collins, F.S., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toohy, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Greenchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Shreen, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 2688)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Dec 19, 2003 this sequence version replaced gi:14424611.
Contact: MGC help desk
Email: cgabps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Sequencing Center: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hghri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lari, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.38% Indels: 0
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US-10-624-932C-2 (1-898) x BC009333 (1-2688)
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1 Kuramoto, T., Kuwamura, M. and Serikawa, T.
Rat neurological mutations cerebellar vermis defect and hobble are caused by mutations in the netrin-1 receptor gene Unc5h3
Brain Res. Mol. Brain Res. 122 (2), 103-108 (2004)
15010202

2 (bases 1 to 9328)
Kuramoto, T. and Serikawa, T.
Direct Submission
Submitted (22-AUG-2003) Takashi Kuramoto, Institute of Laboratory Animals, Graduate School of Medicine, Kyoto University;
Yoshidakono-cho, Sakyo-ku, Kyoto 606-8501, Japan
(E-mail:tkuramoto@anim.med.kyoto-u.ac.jp, Tel:81-75-753-4494, URL:www.anim.med.kyoto-u.ac.jp, Fax:81-75-753-4409)
Fax:81-75-753-4409

Location/Qualifiers
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Job time : 14684 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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SUMMARIES

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27	2845	59.4	2635	11	ADN95100
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34	2563.5	53.5	2860	6	ABT06279
35	2563.5	53.5	2860	6	ABT06280
36	2558.5	53.4	3884	4	AAS21316
37	2558.5	53.4	3884	8	ACA03675
38	2558.5	53.4	3884	8	ABX89213
39	2558.5	53.4	3884	8	ACD41867
40	2558.5	53.4	3884	8	ACA04096
41	2558.5	53.4	3884	9	ADA45664
42	2558.5	53.4	3884	9	ADA76095
43	2558.5	53.4	3884	9	ADA18745
44	2558.5	53.4	3884	9	ADA61368
45	2558.5	53.4	3884	9	ADB19153

ALIGNMENTS

RESULT 1
ABK37922
ID ABK37922 standard; cDNA; 2752 BP.

XX AC ABK37922;

XX DT 21-MAY-2002 (first entry)

XX DE cDNA encoding Human protein NOV1.

XX KW Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; aethma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.

XX OS Homo sapiens.

XX PN WO200210216-A2.

XX PD 07-FEB-2002.

XX PF 30-JUL-2001; 2001WO-US024225.

XX XX

PR 28-JUL-2000; 2000US-0221409P.
 PR 04-AUG-2000; 2000US-0222840P.
 PR 04-AUG-2000; 2000US-0223752P.
 PR 04-AUG-2000; 2000US-0223762P.
 PR 04-AUG-2000; 2000US-0223769P.
 PR 04-AUG-2000; 2000US-0223770P.
 PR 14-AUG-2000; 2000US-0225146P.
 PR 15-AUG-2000; 2000US-0225392P.
 PR 15-AUG-2000; 2000US-0225470P.
 PR 15-AUG-2000; 2000US-0225697P.
 PR 01-FEB-2001; 2001US-0263662P.
 PR 05-APR-2001; 2001US-0281645P.
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
 PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
 XX
 DR WPI; 2002-180074/23.
 DR P-PSDB; AAU85403.
 XX
 PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
 PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
 PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
 PT immune disorders.
 XX
 PS Claim 9; Page 9-10; 213pp; English.
 XX
 CC The invention relates to an isolated cytoplasmic, nuclear, membrane
 CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
 CC form. Also included are the nucleic acids encoding the NOVX proteins, a
 CC vector comprising the nucleic acid, a cell comprising the vector, an anti
 CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
 CC antibody are useful for treating or preventing a NOVX-associated
 CC disorder, where the disorder is selected from cardiomyopathy,
 CC atherosclerosis, diabetes, a disorder related to cell signal processing
 CC and metabolic pathway modulation, metabolic disorders, obesity,
 CC infectious disease, anorexia, cancer-associated cachexia, cancer,
 CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
 CC immune disorders, haematopoietic disorders, and the various
 CC dyslipidaemias, metabolic disturbances associated with obesity, the
 CC metabolic syndrome X and wasting disorders associated with chronic
 CC diseases, bacterial, fungal, protozoal and viral infections, pain,
 CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
 CC disease, multiple sclerosis, Albrit Hereditary Osteodystrophy, angina
 CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
 CC hypertrophy, and psychotic and neurological disorders, including anxiety,
 CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
 CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
 CC nucleic acid is useful in gene therapy. The present sequence encodes a
 CC NOVX protein
 XX

SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1 91e-304 Length: 2752
 Score: 4791.00 Matches: 899
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-624-932C-2 (1-898) x ABK37922 (1-2752)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyValLeuAlaAlaTrpLeu 20
 Db 46 ATGGCGGTCGGGCGCGCTGTGGCCAGCGCTCTCTGGCAGTACTCTCGCGCTTGGCTC 105
 Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
 Db 106 CGCGGTCGGGTGCCAGAGAGTGCACCGTGGCCAAACCCAGTGTGCTGTCACACCCG 165
 Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrileValLysAsnLysPro 60

Db 166 GACCTGCTTCCCACATTCCTGGTGGAGCCCGAGGATGTGTACATCTGTCAAGAAACAGCCA 225
 Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
 Db 226 GTGCTGCTTGTGTCAAGGCGGTGCCCGCCACCGCAGATCTTCTCAAGTGCACGGGGAG 285
 Qy 81 TrpValArgGlnValAspHisValIleGluAArgSerThrAspGlySerSerGlyLeuPro 100
 Db 286 TGGGTGCGCCAGTGGACCACTGATCGAGCGCAGCACAGCGGAGCAGTGGGCTGCC 345
 Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValIleGluValPheGlyLeuGlu 120
 Db 346 ACCATGGAGGTCCGCATTAAATGTCTCAGGCGAGCAGGTGAGAAAGGTGTTCGGGCTGGAG 405
 Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
 Db 406 GAATACTGCTGCCAGTGGCGTGGCATGGAGCTCTCGGGCACCCACCAAGAGTCAGAGGCC 465
 Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
 Db 466 TACATCCGATAGCCAGATTGGCGAAGAACTTCGAGCAGAGCGCTGGCCCAAGGAGTG 525
 Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
 Db 526 TCCTGGAGCAGGGCATCTGCTGCTCCCTCCACCGAGGCGCATCCTCCAGGCGGAG 585
 Qy 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrile 200
 Db 586 GTGGAGTGGCTCCGGAACGAGGACCTGTGTGGACCCGCTCTGGACCCCAATGTATACATC 645
 Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
 Db 646 ACGCGGGAGCACAGCTGTGTGGCAGAGCGCGCTTGTGTGACACGGCCCACTACAC 705
 Qy 221 CysValAlaLysAsnIleValAlaArgArgArgSerAlaSerAlaAlaValIleValTyr 240
 Db 706 TCGTGGCCCAAGAACATCTGGCAGCTGCCGCGCGCTCCGCTCTGTCTATCGTCTAC 765
 Qy 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
 Db 766 GTGAACGGTGGGTGGTGGACGTGGACCGAGTGGTCTGTGACGAGCCAGCTGTGGGCGC 825
 Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAnProAlaProLeuAsnGlyGlyAlaPhe 280
 Db 826 GGTGTGCAAAACGGAGCGGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTC 885
 Qy 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
 Db 886 TGTGAGGGGCGAAGTGTCCAGAAACAGCTGGGCCACCTGTGCCAGTAGACGGCAGC 945
 Qy 301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
 Db 946 TGGAGCCCGTGAGCAAGTGGTCCGCTGTGGCTGGACCTGCACCCACTGGCGGAGCGGT 1005
 Qy 321 GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp 340
 Db 1006 GAGTGTCTGTGACCCAGCACCCCGCAACCGAGGGGAGGAGTGGCAGGGCCTGACCTGGAC 1065
 Qy 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
 Db 1066 ACCCGCACTGTACAGTGACCTCTGTGTACACAGTGTCTTGGCCCTCAGGAGCGTGGCC 1125
 Qy 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
 Db 1126 CTCTATGTGGGCTCATCGCCGTGGCCGTCTGCTGGTCTGCTGTGCTGTGCTCATC 1185
 Qy 381 LeuValTyrCysArgLysGluGlyLeuAspSerAspValAlaAspSerIleLeu 400
 Db 1186 CTCGTTTATTCGGAAGAGGAGGGGCTGAGACTCAGATGTGGCTGACTCGCTCATTC 1245
 Qy 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420

QY 221 CysValAlaIysAenIleValAlaArgArgSerAlaSerAlaValIleValTyr 240
DB TCGTGGCCAAAGAACATCGTGGCAGCTCGCGCAGCGCCCTCCGCTGCTGTCATCTCTAC 765
QY 241 ValAsnGlyGlyTyrSerThrTyrThrGluTyrSerValCysSerAlaSerCysGlyArg 260
DB GTGAACGGTGGTGGTGGAGTGGACCGAGTGGTCTGCTGCGAGCGCCAGCTGTGGGGCG 825
QY 261 GlyTyrGlnIysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
DB GGCTGGCAGAAACGGAGCGGAGCTGCACCAACCCGGGCTCTCAACGGGGGGCGCTTC 885
QY 281 CysGluGlyGlnAsnValGlnIysThrAlaCysAlaThrLeuCysProValAspGlySer 300
DB TGTGAGGGGAGAGATGTCAGMAAACAGCCTGGGCCACCCCTGTGCCCCAGTAGAGCGCAGC 945
QY 301 TrpSerProTrpSerIysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
DB TGGAGCCCGTGGAGCAAGTGGTGGCTGTGGGCTGGACTGCACCCACTGGCGGAGCGGT 1005
QY 321 GluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAsp 340
DB GAGTGTCTGACCCAGCAGACCCCGCAGCGAGGGAGAGTGCACGGGCACTGACCTGGAC 1065
QY 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
DB ACCCGCAACTGATACAGTACCTCTGTGTATACAGTGTCTTCTGGCCCTGAGGAGCGTGGCC 1125
QY 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
DB CTCTATGTGGGCTCATCGCGCTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1185
QY 381 LeuValTyrCysArgIysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeu 400
DB CTGTTTATTGCCGAGAGAGAGGGGCTGAGCTCAGATGTGGTGACTGTCCTCATCTCTC 1245
QY 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
DB ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAGCAGCAACCCCTCTGCTC 1305
QY 421 ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThr 440
DB ACCATCCAGCCGAGCCTCAGCACCACCACCACCACCACCACCACCACCACCACCACCACC 1365
QY 441 GluAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
DB CAGATGGGCCCCAGCCCAAGTTCACCTCACCNAATGGGCACCTGCTCAGCCCCCTGGGT 1425
QY 461 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer 480
DB GGCGGCGCCACACACTGCACACACAGCTCTCCACCTCTCAGGCGGAGGATTCGTCTCC 1485
QY 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
DB CGCTCTCCACCCAGAACTACTTCCTCGCTCCCTGCGCCGAGGCCACCAGCAACATGACCTAT 1545
QY 501 GlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu 520
DB GGGACCTTCAACTCTCTCGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCCCTCTC 1605
QY 521 IleProProAspAlaIleProArgGlyIleIleTyrGluIleTyrLeuThrLeuHisLys 540
DB ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAG 1665
QY 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
DB CCGAAGACGTGAGGTGGTGGCTAGCTGGCTGTGTCAGACCCCTGCTGAGTCCCATCTGTAGC 1725
QY 561 CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
DB TGTGGACCCCTGGCGCTGCTCACCCTGGCCAGTCACTCTGGCTATGGACCACTGTGGG 1785
QY 581 GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp 600

DB 1786 GAGCCAGCCCTGACAGCTGGAGCTGGCGCTCAAAAAGCAGTCGTGGAGGGCAGCTGG 1845
QY 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
DB 1846 GAGGATGTGTGCACTCGGCGAGGAGGCGCCCTCCACCTCTACTACTCCAGCTGGAG 1905
QY 621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
DB 1906 GCCAGTGGCTGCTACGTCTTCAACGAGCAGCTGGCGCGCTTTGCCCTGGTGGAGAGGCC 1965
QY 641 LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr 660
DB 1966 CTCAGCGTGGCTGGCCCAAGCGCTCAAGCTGCTTCTGTTTGGCGGGTGGCTGCACC 2025
QY 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
DB 2026 TCCCTCGAGTACAACTCCGGGTCTACTGCTCGATGACACCCACGATGCACTCAAGAG 2085
QY 681 ValValGlnLeuGlyLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHis 700
DB 2086 GTGGTGCAGCTGGAGAAAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCACGGGTCTGCAC 2145
QY 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
DB 2146 TTCAGGACAGATTACCAACACCTGCGCTATCCATCCACGATGTGCCAGCTCCCTGTGG 2205
QY 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTyrAsnGlyThr 740
DB 2206 AAGAGTAAGTCTCTGTGCTGCTACAGGAGATCCCCCTTTTATCACATCTGGAATGGCAGC 2265
QY 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
DB 2266 CAGCGGTACTTGCACCTGCACCTTCACTCGAGGGGTGTGAGCCCCCAGCCTAGTGACTG 2325
QY 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
DB 2326 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGCAGGGCAGAGCTTCAGCATCAACTTC 2385
QY 781 AsnIleThrLysAspThrArgPheAlaGluLeuAlaLeuLeuLeuLeuLeuLeuLeuLeu 800
DB 2386 AACATCACAAGGACACAAGGTTGTGCTGAGCTCTGCTGCTGAGAGTGAAGCGGGGGTC 2445
QY 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
DB 2446 CAGCCCTGTGGTGGCCCCAGTGTCTTCAGATGCCCTTCTCTCATTCGGCAGAGATTAAT 2505
QY 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
DB 2506 TCCAGCCTGGACCCACCTGTAGCGGGGTGCGACTGGCGGACTCTGGGCCAGAAACTC 2565
QY 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
DB 2566 CACTGGACAGCCATCTCAGCTTCTTTGCTCCAGCCAGCCCCCAGCCATGATCCTC 2625
QY 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
DB 2626 AACCTGTGGAGGGCGGCACTTCCCCACGCGCAACTCAGCCAGCTGGCTGGCAGCAGTG 2685
QY 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
DB 2686 GCTGGAGTGGGCCAGCAGACGCTGGCTCTTTCACAGTGTGGAGGGCTGAGTGC 2739
RESULT 3
ABK52891
ID ABK52891 standard; DNA; 2697 BP.
XX AC
AC ABK52891;
XX AC
DT 27-AUG-2002 (first entry)
XX Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.
XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;
 KW neotropic; neuroprotective; cytoskeletal; antiparkinsonian;
 KW cerebroprotective; cancer; central nervous system; CNS; stroke;
 KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..2697
 FT /tag= a
 FT /product= "Netrin binding membrane receptor UNC5H-1"

XX W0200233080-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-EP011891.

XX 16-OCT-2000; 2000US-0240061P.

XX (FARB) BAYER AG.

XX Koehler RH;

XX WPI; 2002-463314/49.

XX P-PSDB; AAU97899.

XX Novel human netrin binding membrane receptor polypeptide and
 PT polynucleotides for identifying modulating agents useful in treating
 PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
 PT Alzheimer's disease.

XX Claim 1; Fig 1; 94pp; English.

XX This invention relates to the DNA and protein sequences of a novel
 CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
 CC sequence of the invention is useful as a probe for detecting a nucleic
 CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
 CC of the invention are useful to screen for agents which decrease the
 CC activity of the UNC5H-1 protein. The sequences are also useful for
 CC screening agents which regulate (modulate) the activity of the protein of
 CC the invention. A pharmaceutical composition containing the protein of the
 CC invention or a reagent that modulates the activity of the UNC5H-1 protein
 CC may be useful for treating a UNC5H-1 dysfunction related disease such as
 CC cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
 CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
 CC proteins comprising the UNC5H-1 protein are useful for generating
 CC antibodies and for in various assay systems, and the protein can be used
 CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
 CC of the invention is useful for detecting a coding sequence for the UNC5H-
 CC 1 protein. The present sequence represents a DNA sequence encoding the
 CC human netrin binding membrane receptor UNC5H-1 protein of the invention

XX Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	8,43e-304	Length:	2697
Score:	4781.00	Matches:	896
Percent Similarity:	99.89%	Conservative:	1
Best Local Similarity:	99.78%	Mismatches:	0
Query Match:	99.79%	Indels:	0
DB:	6	Gaps:	0

US-10-624-932c-2 (1-898) x ABK52891 (1-2697)

QY	1	MetAlaValArgProGlyLeuTTPProAlaLeuLeuGlyTleValLeuAlaAaTTPLeu	20
DB	1	ATGCGCGTCCGGCCCGCCCTGTGGCCAGCGCTCTCTGGGCATAGTCTCTGCCCGCTTGGCTC	60
QY	21	ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro	40
DB	61	CGCGGCTCGGGTCCCGCAGCAGAGTGCACCGTGGCCAAACCCAGTCTGTGTGGTCCAAACCG	120

QY	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro	60
DB	121	GACCTGCTCCCCACTTCTCGTGTGGAGCCCGAGGATGTGTACATCGTCAAGAAACAAGCCA	180
QY	61	ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu	80
DB	181	GTGCTGCTTGTGTGCAAGCCGCTGCCCGCCACAGATCTTCTCAAGTCAACGGGGAG	240
QY	81	TTPValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro	100
DB	241	TGGGTGGCCAGGTGGACCAACGATCGAGCGCAGCACAGCGGAGCAGTGGGCTGCC	300
QY	101	ThrMetGluValArgIleAsnValSerArgGlnGlnValGlnLysValPheGlyLeuGlu	120
DB	301	ACCATGGAGTCCGCAATTAATGTCTCAAGGCAGCAGTCCAGAAAGGTGTTCGGGCTGGAG	360
QY	121	GluTyrTrpCysGlnCysValAlaThrSerSerGlyThrThrLysSerGlnLysAla	140
DB	361	GAATACCTGGTCCAGTGGCATGGAGTCTCCGGGCACCAACCAAGAGTCAAGAAGGCC	420
QY	141	TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal	160
DB	421	TACATCCGCATAGCCTATTTCGCAAGAACTTCGAGCAGAGCGCTGGCCAAAGGAGTG	480
QY	161	SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu	180
DB	481	TCCCTGGAGCAGGGCATCGTGTGCTGCCCTCCGTCACCGGAGGSCATCCCTCCAGCCGAG	540
QY	181	ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle	200
DB	541	GTGGAGTGGCTCCGGAACGAGGACCTGTGTGGACCCCTCCCTGGACCCCAATGTATACATC	600
QY	201	ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr	220
DB	601	ACGCGGGAGCAGACCGCTGTGTGTGTCAGAGCCCGCTTGTGTGACACGCGCAACTACACC	660
QY	221	CysValAlaLysAsnIleValAlaArgArgArgSerAlaSerAlaAlaValIleValTyr	240
DB	661	TGCGTGGCCCAAGAACATCGTGCACGTCCGCGCAGCGCTCCGCTCTGTCTCATCTGTCTAC	720
QY	241	ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg	260
DB	721	GTGACCGTGGTGGTGTGCGCTGGACCGAGTGGTCTGTGTCAGCGCCAGCTGTGGGCGC	780
QY	261	GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe	280
DB	781	GGCTGGCAGAAACGGAGCCGAGCTGCACCAACCCGCGCTCTCAACCGGGGCGCTTTC	840
QY	281	CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer	300
DB	841	TGTGAGGGGCGAGAAATGTCCAGAAACAGCTGGCCACCTGTGGCCAGTGGGACGGCAGC	900
QY	301	TTPSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg	320
DB	901	TGGAGCCCGTGGAGCAAGTGGTGGCTGTGGCTGGATGGACACCCACTGGCGGAGCCGT	960
QY	321	GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp	340
DB	961	GAGTGTCTGTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGGCCAGGCGCACTGACCTGGAC	1020
QY	341	ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla	360
DB	1021	ACCCGCAACTGTACCACTCTGTGTGTACACACTGTCTGTGGCTTGTGGCGCTGGAGCGTGGCC	1080
QY	361	LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle	380
DB	1081	CTCTATGTGGGCTCATCGCCGTGGCCGTCTGCTGTCTCTGTCTGTCTCTCTCTCTCTCTCT	1140
QY	381	LeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeu	400
DB	1141	CTCGTTTATTGGCGAAGAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCTCATTTCTC	1200
QY	401	ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu	420

CC signal processing and metabolic pathway modulation, in a human. Detecting
CC the polypeptide or polynucleotide is useful for identifying cancerous
CC tissue. The antibody can be used to treat diabetes or cancer. The host
CC cells can be used to produce non-human transgenic animals useful in drug
CC screening. The present nucleic acid sequence is that of the human UNC5-
CC like NOV1 gene located on chromosome 13. This sequence encodes the human
CC UNC5-like protein NOV1 of the invention
XX
SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,36e-298 Length: 2881
Score: 4698.50 Matches: 888
Percent Similarity: 98.89% Conservative: 2
Best Local Similarity: 98.67% Mismatches: 7
Query Match: 98.07% Indels: 3
DB: 6 Gaps: 3

US-10-624-932C-2 (1-898) x ABK49422 (1-2881)

QY 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyLeValLeuAlaLaTrpLeu 20
DB 87 ATGGCGGTCCGGCCCGCGCTGTGGCCAGCGCTCTGGGCATAGTCTCTCGCCGCTTGGCTC 146
QY 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAAsnPro 40
DB 147 CGCGGCTCGGGTCCCGACAGAGTGCACCCTGGCCCAACCCAGTGCCTGGTGCACACCCG 206
QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrileVallysAsnLysPro 60
DB 207 GACCTGCTTCCCCACTTCTCGTGGAGCCCGAGGATGTACATCGTCAAGAACAGCCCA 266
QY 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
DB 267 GTGCTGCTGTGTGCAAGCGGTGCGCCGCCACGACAGATCTTCTCAAGTGCACCGGGAG 326
QY 81 TrpValArgGlnValAAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
DB 327 TGGGTGGCCAGGTGGACCAACGATGTCAGCGCAGCAGACAGCGGAGCAGTGTGTAGCCG 386
QY 101 ThrMetGluValArgIleAAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
DB 387 ACCATGGAGGTCCGCATTATGTCTCAAGCAGCAGGTCCGAAAGGTGTTCGGGCTGGAG 446
QY 121 GluTyrTrpCysGlnCysValAlaLaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
DB 447 GAATACTGTGGTCCAGTGCCTGGTGGATGGAGCTCTCCGGGCACACCACAGAGTCAGAAGGCC 506
QY 141 TyrIleArgIleAlaArgLeuArgLysAAsnPheGluGlnProLeuAlaLysGluVal 160
DB 507 TACATCGCATAGCCAGATTGCCAAGAATTCGAGCAGAGCCGCTGGCCAAAGGAGGTG 566
QY 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
DB 567 TCCCTGGAGCAGGCGATCGTGCCTGCCCTGCCAGCGAGGGCATCCCTCCAGCCGAG 626
QY 181 ValGluTrpLeuArgGlnAspLeuValAspProSerLeuAspProAsnValTyrile 200
DB 627 GTGGAGTGGTCCGGAAACGAGGACCTGGTGGACCCGCTCCCTGACGCCCAACTATACATC 686
QY 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
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QY 221 CysValAlaLysAAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
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DB 867 GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCCGCGCTCTCAACCGGGCGCTTTC 926
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QY 380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAAspSerSerIle 399
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PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Bainger SR, Ellerman K;
PI Ectenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkete RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71610.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 505; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipase activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
XX Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2,36e-298 Length: 2881
Score: 4698.50 Matches: 888
Percent Similarity: 98.89% Conservative: 2
Best Local Similarity: 98.67% Mismatches: 7
Query Match: 98.07% Indels: 3
DB: 12 Gaps: 3
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Qy 520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
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Qy 859 IleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAla 878
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ID ADH71627 standard; DNA; 2881 BP.
XX
AC ADH71627;
XX
XX 25-MAR-2004 (first entry)
DT
XX
XX Human gene of the invention NOV21j SEQ ID NO:523.
DE
XX
XX db; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
XX WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
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PR 05-JUN-2002; 2002US-0386047P.
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PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
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PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 07-JUN-2002; 2002US-0387535P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387688P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
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PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.

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RESULT 8
ADH71641
ID ADH71641 standard; DNA; 2881 BP.
AC ADH71641;
XX
XX 25-MAR-2004 (first entry)
DT Human gene of the invention NOV21q SEQ ID NO:537.
XX
DE ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
PF
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
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PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR

PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71642.
DR
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 537; 1880pp; English.
PS
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC

CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOVX polypeptide of the invention.

XX
 SQ Sequence 2881 BP; 526 A; 986 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,71e-298 Length: 2881
 Score: 4695.50 Matches: 887
 Percent Similarity: 98.89% Conservative: 3
 Best Local Similarity: 98.56% Mismatches: 7
 Query Match: 98.01% Indels: 3
 DB: 12 Gaps: 3

US-10-624-932C-2 (1-898) x ADH71641 (1-2881)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeu 20
 Db 87 ATGGCCGTCCGGCCCGCGCTGTGGCCAGCGCTCTCTGGGCATAGTCTTCGCCGCTTGGCTC 146
 Qy 21 ArgGlySerGlyAlaGlnSerAlaThrValAlaAlaAsnProValProGlyAlaAsnPro 40
 Db 147 CGCGGCTCGGGTGCAGCAGAGTGCCACCGTGCCCAACCCAGTGCCTGGTGCCACCCCG 206
 Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
 Db 207 GACCTGTCTCCCACTTCTCTGGTGAGCCCGGAGGATGTATACATCGTCAAGAACCAAGCCA 266
 Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
 Db 267 GTGCTGTGTGTGCAAGCCGCTGCCCGCCACGAGATCTTCTCAAGTGCAACGGGGAG 326
 Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
 Db 327 TGGGTGCGCCAGTGGACACGTCATCGAGCGCAGCAGACGCGGAGCAGTGTGTGAGCCG 386
 Qy 101 ThrMetGluValArgIleAsnValSerArgGlnValGluLysValPheGlyLeuGlu 120
 Db 387 ACCATGGAGGTCCGATTAATGTCTCAAGGCAGCAGGTTCGAGAAAGGTGTTCGGGCTGGAG 446
 Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
 Db 447 GAATACTGTGTGCCAGTGTGGCATGAGTCTCTCGGGCACCAAGAGTCAAGAGGCC 506
 Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
 Db 507 TACATCCGATAGCCAGATGGCGAAGAACTTCGAGCAGAGCGCGCTGGCCAGAGAGTG 566
 Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
 Db 567 TCCCTGGAGCAGGAGCATCGTGTCTCCCTGCGCTCACCGGAGGCGATCCCTCCAGCCGAG 626
 Qy 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
 Db 627 GTGAGTGTGCTCCGGALACGAGGACTGTGTGACCCGCTTCCTGGACCCCAATGTATATCATC 686
 Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
 Db 687 ACGCGGAGCAGACGCTGTGTGGCAGACGCGCCGCTTGTGTGACAGCGCCCACTACACC 746
 Qy 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaValIleValTyr 240
 Db 747 TGGGTGGCCAAAGAACATCGTGGCAGCTCGCGCAGCGCCTCCGCTGTGTCTATCGTCTAC 806

Qy 241 ValAsnGlyGlyTyrTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyValArg 260
 Db 807 GTGACCGGTGGTGGTGTGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGCGC 866
 Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
 Db 867 GGCTGGCAGAAACGAGAGCGAGGTGACCAACCGCGCGCTCTCAACGGGGGCGCTTTC 926
 Qy 281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
 Db 927 TGTGAGGGGAGAGATGTCATGACCCGACCGTCTCTCTCTGTGTGTCTCTGTGTGAGCGC 986
 Qy 300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
 Db 987 AGCTGGAGCCCGTGGAGCAAGTGGTGGCTGTGGGTGGAGTGCACCCACTGCGGGAGC 1046
 Qy 320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 339
 Db 1047 CGTGAGTGTCTTGACCCAGCACCCCGCAACGAGGGGAGGAGTGCACGGGCACTGACCTG 1106
 Qy 340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
 Db 1107 GACACCCGCAACTGTACCACTGACCTCTGTGTACACAGTGTCTTGGCCCTTGAGGAGCTG 1166
 Qy 360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
 Db 1167 GCCTCTATGTGTGGGCTCATCGCGTGGCGCTGTGCTGTGTGTGTGTGTGTGTGTGT 1226
 Qy 380 IleLeuValTyrCysArgLysGlyGluGlyLeuAspSerAspValAlaAspSerSerIle 399
 Db 1227 ATCTCGTATTTATTCGCGAAGAGGAGGGCTGAGACTCAGATGTGGTGTGACTGTCCATT 1286
 Qy 400 LeuThrSerGlyPheGlnProValSerIleIysPheSerLysAlaAspAsnProHisLeu 419
 Db 1287 CTCACTCTCAGGCTTCCAGCCCGCTCAGCATCAAGCCCAAGAGCAGCAACCCCATCTG 1346
 Qy 420 LeuThrIleGlnProAspLeuSerThrThrThrThrTyrTyrGlnGlySerLeuCysPro 439
 Db 1347 CTACACCATCCAGCGGACCTCAGC---ACCACCACTCTACAGGGGAGTCTCTGTCCC 1403
 Qy 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeu 459
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 Db 1464 GGTGGCGCGCCGACACACTGCACCACTCTCCCACTCTCAGGGCCGAGGATTCGTC 1523
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 Db 1524 TCCGCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCGAGGACAGCAGCAATGACC 1583
 Qy 500 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
 Db 1584 TATGGACCTTCACTCTCGGGGCGGCTGATGATCCCTAATACAGGTATCAGCCTC 1643
 Qy 520 LeuIleProProAspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHis 539
 Db 1644 CTATCCCCCAGATCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTCAGC 1703
 Qy 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
 Db 1704 AACCCGGAAGACGTGAGTGTGCCCTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1763
 Qy 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
 Db 1764 AGCTGTGGACCCCTGGCGTCTGTCTCACCAGCCAGTCTATCTGGCTATGGACCACTGT 1823
 Qy 580 GlyGluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySer 599
 Db 1824 GGGGAGCCCGCTGACAGCTGAGCGCTCGCGCTCAAAAGAGCAGTGTGTGCGGGGAGC 1883

221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaValIleValTyr 240
747 TGGTGGCCAAAGAACATCGTGGGCACAGTGGCGGAGCGCTCCCGCTGCTGCATCGTCTAC 806
241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
807 GTGAACGGTGGTGGTGCAGTCGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGCGC 866
261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPhe 280
867 GGCTGGCAGAAACGAGCGCGAGCTGCACCAACCCGCGCTCTCAACGGGGCGCTTC 926
281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
927 TGTGAGGGGAGAATGTCCATGACCGACCGTCTCTCTGCTGTCTGTGGACGGC 986
300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
987 AGCTGGAGCCCGTGGAGCAAGTGGTGGCTGTGGCTGGACTGCACCCACTGGCGGAGC 1046
320 ArgGluCysSerAspProAlaProArgAsnGlyGluGluCysGlnGlyThrAspLeu 339
1047 CGTGAGTGTCTCAACCCAGCACCCCGCAACGAGGGGAGGAGTGCAGGGCACTGACCTG 1106
340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
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360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
1167 GCCCTCTATGTGGCCTCATCGCGCGTGGCGCTGTGCTGTGCTGTGCTGCTCCTC 1226
380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerIle 399
1227 ATCTCTGTTATTTCGCGGAAGAGGAGGGCTGGACTCAGATGTGGCTGACTCGTCCATT 1286
400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
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440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuSerProLeu 459
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1584 TATGGACCTTCAACTCTCTCGGGGGCGCGCTGATGATCCCTAATACAGGTATCAGCCTC 1643
520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
1644 CTCATCCCCCAGATGCCATACCCCGAGGAAGATCTATGAGATCTACCTCAGCGCTGCAC 1703
540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
1704 AAGCCGAAGACGTGAGGTGGCCCTAGCTGGCTGTGCAGACCTGTGCTGAGTCCCATCGTT 1763
560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
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1824 GGGGAGCCAGCCCTGCAGAGCTGGAGCCTCGCGCTCAAAAGAGAGTCTGTCGAGGGGAGC 1883
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619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
1944 CTGGAGCCAGTGCCTGTCTACGTCTTACCAGGACAGCTGGCGCGCTTGTCCCTGTGGGA 2003
639 GluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuPheAlaProValAla 658
2004 GAGGCCCTCAGCGTGGCTGCCAACAGCGCTCAAGCTCTCTGTGTGGCGCGGTGCC 2063
659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
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679 LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgVal 698
2124 AAGGAGTGTGCAGCTGGAGAGCAGCTGGGGGACAGCTATCCAGGAGCCACGGTCC 2183
699 LeuHisPheLysAspSerTyrHisLeuLeuArgLeuSerIleHisAspValProSerSer 718
2184 CTGCATCTCAAGACAGTATACCAACCTGGCGCTATCCATCCAGATGTGCCAGCTCC 2243
719 LeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsn 738
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759 AspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIle 778
2364 GACCTGGCCTGCAGCTGTGGGTGTGGAGGTGGAGGGGAGCGGGGAGAGCTTCAGCATC 2423
779 AsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAla 798
2424 AACTTCAACATCACCAAGGACACAAGGTTTGTCTGAGCTGTGGCTCTGGAGAGTGAAGCG 2483
799 GlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLys 818
2484 GGGGTCCCAAGCCCTGGTGGGCCCCAGTGCCTTTCAGATCCCTTCTCATTCGGCAGAAG 2543
819 IleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGln 838
2544 ATAAATTCAGGCTGGACCCACCTGTAGCGGGGTGCCGACTGGCGGAGCTCTGGGCCAG 2603
839 LysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThrAlaMet 858
2604 AAATCCACCTGGACAGCATCTCAGCTTCTTTGCTCCAGCCAGCCAGCCCCACAGCATG 2663
859 IleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAla 878
2664 ATCTCTCAACTGTGGAGCGCGCACTTCCCAACGCGCAACCTCAGCCAGCTGGGTGCA 2723
879 AlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValIleSerGluAlaGluCys 898
2724 GCAGTGGCTGGACTGGGCCAGCCAGCAGCTGGCCTCTTTCACAGTGTCCGAGGCTGAGTGC 2783
RESULT 11
ADH71631
ID ADH71631 standard; DNA; 2881 BP.
XX
AC ADH71631;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV211 SEQ ID NO:527.
XX

KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX Homo sapiens.

OS WO2003102155-A2.

PN 11-DEC-2003.

PD 03-JUN-2003; 2003WO-US017430.

PF 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 06-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 07-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0236960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388036P.

PR 13-JUN-2002; 2002US-0389123P.

PR 13-JUN-2002; 2002US-0389118P.

PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.

PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.

XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Etenberg S, Gangollil EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;

XX WPI; 2004-081935/08.

DR P-PSDB; ADH71632.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 527; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2881 BP; 526 A; 984 C; 868 G; 503 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.32e-298 Length: 2881
Score: 4694.50 Matches: 887
Percent Similarity: 98.78% Conservative: 2
Best Local Similarity: 98.56% Mismatches: 8
Query Match: 97.99% Indels: 3
DB: 12 Gaps: 3

US-10-624-932C-2 (1-898) x ADH71631 (1-2881)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaTrpLeu 20
Db 87 ATGGCCGTCGGCCCGCCCTGTGGCCAGCGCTCTCTGGCATAGTCTCTGGCGGTGGCTC 146
Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40

147 CGCGGCTCGGGTCCCGCAGCAGATGCCACCGTGGCCAAACCCAGTGCTGGTGCACACCG 206
Qy
41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValIysAsnLysPro 60
Db
207 GACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGGATGTGTACATCTGTCAAGAAACAAGCCA 266
Qy
61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db
267 GTGCTGCTTGTGTGCAAGCCGTCGCCGCCACGACATCTTCTCAAGTGCACACGGGGAG 326
Qy
81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db
327 TGGGTGGCCAGGTGGACCACTGTATCGAGCGCAGCAGACCGGGAGCAGTGTGTAGCCG 386
Qy
101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGlnLysValPheGlyLeuGlu 120
Db
387 ACCATGGAGTCCGGCATTAATGTCTCAAGGCAGCAGTCCAGAGGAGTGTTCGGGCTGGAG 446
Qy
121 GluTyrTrpCysGlnCysValAlaTyrSerSerSerGlyThrThrLysSerGlnLysAla 140
Db
447 GAATACTGGTGGCAGTGGCGTGGCATGGAGCTCTCGGGCACCAACAGAGTCAAGAGGCC 506
Qy
141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
Db
507 TACATCCGCATAGCCAGATTGCCAGAACTTCGACGAGAGCCGCTGGCCAAAGAGGTG 566
Qy
161 SerLeuGlnGlnGlyIleValLeuProCysArgProProGluGlyIleProAlaGlu 180
Db
567 TCCCTGGAGCAGGCGCATCTGTGCTGCGCTGCCGTCACCGAGGGCATCCCTCCAGCCGAG 626
Qy
181 ValGluTrpLeuArgGlnLeuValAspLeuValAspProSerLeuAspProAsnValTyrIle 200
Db
627 GTGGAGTGGCTCCGGAAACAGGACCTGGTGGAGCCCTGCTGGACCCCAATGTATACATC 686
Qy
201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db
687 ACCGGGAGCAGACCTGGTGGTGGCAGAGGCCCGCTTGCTGACACGGCCAACTACACC 746
Qy
221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
Db
747 TGGCTGGCCAAAGAACATCTGTGGCAGCTCGCGCAGCGCCCTCCGCTGCTGTATCGTCTAC 806
Qy
241 ValAsnGlyGlyTrpSerThrTrpGluTrpSerValCysSerAlaSerCysGlyArg 260
Db
807 GTAAACGGTGGGTGGTGGAGCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 866
Qy
261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
Db
867 GGCTGCGAGAAACGGAGCCGGAGCTGCACCAACCCCGCGCCCTCTCAACGGGGGGCGTTTC 926
Qy
281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
Db
927 TGTGAGGGGAGAAATGTCATGACCGCAGCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 986
Qy
300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
Db
987 AGCTGAGAGCCGTGGAGCAAGTGGTGGGCTGTGGGCTGGAGCTGCACCCACCTGGCGGAGC 1046
Qy
320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 339
Db
1047 CGTGAGTGTCTTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCACGGGCACCTGACCTG 1106
Qy
340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
Db
1107 GACACCGCAACTGTACAGTACCTCTGTGTACACAGTGTCTTGGCCCTCGAGGACGTG 1166
Qy
360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
Db
1167 GCCCTATATGGGCCCTCATGGCCGTGGCCGCTGCTGGTCTGTGCTGTGTGCTGCTGCT 1226
Qy
380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIle 399
Db
1227 ATCCTCGTTTATTGCCGGAAGAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT 1286

Qy
400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
Db
1287 CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCGCAGCAAGCAGCAACCCCATCTG 1346
Qy
420 LeuThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr 439
Db
1347 CTCACCATCCAGCGGACCTCAGC---ACCACCCACACCTTACAGGGCAGTCTCTGTGCC 1403
Qy
440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuLeuSerProLeu 459
Db
1404 CGGCAAGATGGGCCCGCCAGCTTCCAGTTCAGCTACCAATGGGCACTGTGTAGCCCGCTG 1463
Qy
460 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
Db
1464 GGTGGCGGCGGCACACACTGCACACACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC 1523
Qy
480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
Db
1524 TCCCGCTCTCTCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCCACCAAGCAACATGACC 1583
Qy
500 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
Db
1584 TATGGGACCTTCAACTTCTCGGGGCGCGCTGATGATCCCTAATACAGGTATCAGCCCTC 1643
Qy
520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
Db
1644 CTCATCCCCCAGATGTCTATACCCGAGGGAAGATCTATGAGATCTTACCTCAGCGTGCAC 1703
Qy
540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
Db
1704 AAGCCGGAAGAGTGGAGTGGCTGTAGCTGGCTGTGACACCTGTGATGCCATCGTT 1763
Qy
560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
Db
1764 AGCTGTGGACCCCTGGCGTCTGTCTCACCCGCGCAGTCATCTGGCTATGACCACTGT 1823
Qy
580 GlyGluProSerProAspSerTrpSerLeuArgLeuLysGlyGlnSerCysGluGlySer 599
Db
1824 GGGGAGCCCGAGCCCTGACAGCTGAGCGCTGCGCCTCAAAAGCAGTGTGTGCGAGGGCAGC 1883
Qy
600 TrpGlu---AspValIleHisLeuGlyGluAlaProSerHisLeuTyrTrpCysGln 618
Db
1884 TGGAGAGAGATGTGTGCACCTGGCGGAGGAGGCGCCCTCCACCTCTACTACTGCCAG 1943
Qy
619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
Db
1944 CTGGAGCCAGTGCCTGTCTTCTCACCGAGCAGCTGGGCGCTTTTCCCTGTGGTGGGA 2003
Qy
639 GluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAla 658
Db
2004 GAGGCCCTCAGCGTGGCTGCCCGCAAGCGCTCAAGCTCTTCTGTTTGGCGGGTGGCC 2063
Qy
659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
Db
2064 TGCACCTCTCCGTGAGTACAACTCCGGTCTACTGCTGCATGACACCCACCATGACATC 2123
Qy
679 LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnLeuProArgVal 698
Db
2124 AAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCACGGGTC 2183
Qy
699 LeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSer 718
Db
2184 CTGCATTTCAAGGAGAGATTACCAACCTCGCCCTTATCCATCCAGATGTGCCAGCTCC 2243
Qy
719 LeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsn 738
Db
2244 CTGTGGAAGAGTAACTCTTGTGAGCTACCAAGGAGATCCCCCTTTTATCACAATCTGGAAT 2303
Qy
739 GlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSer 758
Db
2304 GGCACGCGCGGTACTTGCATCTGCACCTTACCCCTGGAGCGGTGTAGCCCGCAGCACTAGT 2363

PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 21; SEQ ID NO 529; 1880pp; English.
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing, the
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2880 BP; 527 A; 984 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5,02e-298 Length: 2880
Score: 4693.50 Matches: 887
Percent Similarity: 98.78% Conservative: 2
Best Local Similarity: 98.56% Mismatches: 8
Query Match: 97.96% Indels: 3
DB: 12 Gaps: 3

US-10-624-932C-2 (1-898) x ADH71633 (1-2880)

QY 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyLeValLeuAlaLaTrpLeu 20
DB 86 ATGGCGCTCCGGCCCGGCTGTGGCAGCGCTCTGGCAGATAGTCTCGCGCTTGGCTC 145
QY 21 ArgGlySerGlyAlaGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
DB 146 CGCGCTCGGGTCCCGACGAGATGCCCGTGGCCAAACCGATGCTGTGTCACACCG 205
QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValIysAsnLysPro 60
DB 206 GACCTGCTTCCCCACCTTCCTGGTGGAGCCGAGGATGTATCATCGTCAAGAACAGCCA 265
QY 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
DB 266 GTGCTGCTTGTGTGCAAGGCGGTGCCCGCCACGACAGATCTTCTCAAGTGTCAACGGGGAG 325
QY 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
DB 326 TGGGTGGCCAGGTGGACCACTGATCGAGCGCAGCACACGGGAGCAGTGTGTGAGCCG 395
QY 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
DB 386 ACCATGGAGGTCCGCATTATGTCTCAAGGACAGAGTTCGAGAGGTTCGGGCTGGAG 445
QY 121 GluTyrTrpCysGlnCysValAlaLaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
DB 446 GAATACTGTGTGCCAGTGGTGGATGGAGTCTCGGGCACCAACCAAGAGTCAAGAGGCC 505
QY 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
DB 506 TACATCCGATACCGAATTGCCAGAACTTCGAGCAGGAGCCGCTGGCCAAAGGAGGTG 565
QY 161 SerLeuGluGlnGlyLeValLeuProCysArgProProGlyIleProProAlaGlu 180
DB 566 TCCCTGGAGCAGGGATCGTGTGCTGCCCTGCCGTCACCGGAGGGCATCCCTCCAGCCGAG 625
QY 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
DB 626 GTGGAGTGGCTCCGGAAACGAGGACCTGGTGGACCGCTCCCTGGACCCCAATGTATATC 695
QY 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220

DB 686 ACCTGGGAGCAGCGCTGGTGGTGACAGGCCCGCTTCTGTACAGCGGCAACTACCC 745
QY 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
DB 746 TGGCTGGCCCAAGAACAATCGTGGCACGTGCGCGCAGCGCTTCCGCTGTGTATCGTCTAC 805
QY 241 ValAsnGlyClyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
DB 806 GTGAACCGTGGGTGGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGCGGC 865
QY 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
DB 866 GGTGGCAGAAACGAGCGAGGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTC 925
QY 281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
DB 926 TGTGAGGGGCGAGAATGTCCATGACCGCACCGTCTCTCTCTGTGTGTGGACGCGC 985
QY 300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
DB 986 AGCTGGAGCCCGTGGAGCAAGTGTGGCTGTGGCTGTGACTGCACCCACCTGGCGGAGC 1045
QY 320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 339
DB 1046 CGTGAAGTGTCTGACCCAGCACCCCGCAACGGAGGGGAGAGTGCAGGGGACTGACCTG 1105
QY 340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
DB 1106 GACACCGCGCAACTGTATACAGTACCTCTGTGTACACAGTGTCTTGGCCCTGAGGAGCTG 1165
QY 360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
DB 1166 GCGCTCTATGTGGCGCTCATCGCGTGGCGCTGTGCTGTGCTGTGTGTGTGCTC 1225
QY 380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIle 399
DB 1226 ATCTCTGTTTATTTGCCGGAAGAGAGGGGTGGACTCAGATGTGCTGTACTGTCTCAT 1285
QY 400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
DB 1286 CTCACCTCAGGCTTCCAGCCCGTGCAGCTCAAGCCAGCAAGCAGACCAACCCCATCTG 1345
QY 420 LeuThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThr 439
DB 1346 CTCACCATCCAGCGGACCTCAGC---ACCACCAACCTTACCAGGGCAGTCTCTGTGCC 1402
QY 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeu 459
DB 1403 CGGCAGAGTGGGCCCGCCAGCTTCCAGCTCACCAGTGGGACCTGTGTGAGCCCGCTG 1462
QY 460 GlyGlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
DB 1463 GGTGGCGGCGCCACACACTGCACACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC 1522
QY 480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
DB 1523 TCCCGCTCTCCACCCAGAACTACTTCCGCTCCCTCCCGGAGGCCAGCAGCAACATGACC 1582
QY 500 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
DB 1583 TATGGACCTTCACTTCTCCGGGGCCCGCTGTAGTATCCCTAATACAGGTATCAGCCCTC 1642
QY 520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
DB 1643 CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTATCCTCAGCGTGCAC 1702
QY 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
DB 1703 AAGCCGGAAGAGCTGAGGTGGCCCTAGCTGGCTGTGACACCTCTGTGATGCCATCGTT 1762
QY 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579

PR 15-AUG-2002; 2002US-0403617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-0423798.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425453P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ,
 PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K,
 PI Etenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X,
 PI Gusev V, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR,
 PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS,
 PI Padigaru M, Patturajan M, Pena CB, Peyman JA, Raha D, Rastelli L,
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA,
 PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
 PI Zhong H;
 XX
 DR WPI; 2004-081935/08.
 DR P-PSDB; ADH71630.
 XX
 PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 21; SEQ ID NO 525; 1880pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator, A
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipaeamic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOVX polypeptide of the invention.
 XX
 SQ Sequence 2881 BP; 526 A; 986 C; 868 G; 501 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6-79e-298 Length: 2881
 Score: 4691.50 Matches: 887
 Percent Similarity: 98.78% Conservative: 2
 Best Local Similarity: 98.56% Mismatches: 8
 Query Match: 97.92% Indels: 3
 DB: 12 Gaps: 3

US-10-624-932c-2 (1-898) x ADH71629 (1-2881)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyValLeuAlaAlaTrpLeu 20
 Db ATGGCGGTCGGGCGCGCTTGGCGAGCGCTCTGGGCATAGTCTCGCGGCTGGCTC 146

Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
 Db CGCGGCTCGGGTGGCCAGCAGAGTGCCACCGTGGCCAAACCCAGTGGCTGGTGCACCCG 206
 Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValIleAsnLeuPro 60
 Db GACCTGCTTCCCCACTTCTGTGGAGCCCGAGGATGTGTACATCTCTCAAGAACAGGCCA 266
 Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
 Db GTGCTGCTGTGTGCAAGGCCGTGCCCGCCACCGCAGATCTTCTCAAGTGCACCGGGAG 326
 Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
 Db TGGGTGCGCCAGGTGCACCGATCGATCGAGCGCAGCACAGACGGGAGCAGTGGTGAGCCG 386
 Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
 Db ACCATGGAGGTCCGCATTAAATGTCTCAAGGAGCAGGTGAGAAGGTGTTCTGGGCTGGAG 446
 Qy 121 GluTyrTrpCysGlnCysValAlaAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
 Db GAATACTGGTGCCAGTGGCTGGCATGGAGCTCTCTGGGCACCCACCAAGAGTCAGAGGCC 506
 Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
 Db TACATCCGATAGCCAGATTTGGCAAGAACTTTGAGCAGGAGCGCTGGCCCAAGGAGGTG 566
 Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
 Db TCCCTGGACAGGGCATCTGTCTCCCTGCCGTCCACGGAGGGCATCCTCCAGCCGAG 626
 Qy 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
 Db GTGGAGTGGCTCCGGAACGAGGACCTGTGTGGACCCGCTCCCTGGACCCCAATGTATACATC 686
 Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
 Db ACGCGGGAGCAGAGCCTGGTGGTGACAGAGCGCCCTTTGCTGACACGGCCCACTACACC 746
 Qy 221 CysValAlaLysAsnIleValAlaArgArgArgSerAlaSerAlaAlaValIleValTyr 240
 Db TCGTGGCCCAAGAACATCTGGCACTGCCGAGCGCCCTCCGCTGCTGTCTATCTGCTAC 806
 Qy 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
 Db GTGAACGGTGGGTGGTGGACCGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGGCG 866
 Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPhe 280
 Db GGCTGGCAAAACGGAGCGGAGCTGCACCAACCGCGCCCTCTCAACCGGGGCGCTTTC 926
 Qy 281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
 Db TGTGAGGGGCAGAAAGTTCATGACCGCAGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 986
 Qy 300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
 Db AGCTGGAGCCCGTGGAGCAAGTGGTGGGCTGTGGGCTGGAGCTGGACCCACCGAGCG 1046
 Qy 320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 339
 Db CGTGTGCTCTGTGACCCAGCACCAGGAGGGGAGGAGTGCAGGGGCGCTGACCTG 1106
 Qy 340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
 Db GACACCGCACTGTACACAGTGCCTCTGTGTACACAGTGTCTCTGTGGCCCTGAGGAGCTG 1166
 Qy 360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
 Db GGCCTCTATGTGGGCTCTATCGCCGTGGCGGTCTGTCTGTGTGTGTGTGTGTGTGTGTGT 1226


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PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 11-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-03889123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
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PR 26-AUG-2002; 2002US-0406182P.
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PR 12-SEP-2002; 2002US-0410084P.
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PR 23-SEP-2002; 2002US-0412731P.
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PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414940P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
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PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangoli EH, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Pattarajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
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XX WPI; 2004-081935/08.
DR P-PSDB; ADH71644.
DR
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XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 539; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipase activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.79e-298 Length: 2881
Score: 4691.50 Matches: 887
Percent Similarity: 98.78% Conservative: 2
Best Local Similarity: 98.56% Mismatches: 8
Query Match: 97.92% Indels: 3
DB: 12 Gaps: 3

US-10-624-932C-2 (1-898) x ADH71643 (1-2881)

QY 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyValLeuAlaAlaTrpLeu 20
Db 87 ATGGCCGTCGGCCCGCCCTGTGGCCAGCGCTCTGGGCATAGTCTCGCCGCTTGGCTC 146
QY 21 ArgGlySerGlyAlaGlnGlnSerAlaThrAlaAlaAsnProValProGlyAlaAsnPro 40
Db 147 CGCGGCTCGGGTGGCCAGCAGAGTGCCACCGTGGCCACCCAGTGCTGTGCAACCCG 206
QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValIleAsnLysPro 60
Db 207 GACCTGCTTCCGACCTTCTGTGGAGCCGAGGATGTATCATCTCTAAGAACAGCA 266
QY 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db 267 GTGCTGCTGTGTGCAGGCCGCTGCCCCGCCAGCATCTTTCTCAAGTGCACGGGGAG 326
QY 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 327 TGGGTGGCCAGGTGGACCCAGCTGATCGAGCGCAGCAGACGAGGAGCAGTGGTGAGCCG 386
QY 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 387 ACCATGGAGGTCCGCAATTAATGTCTCAAGCAGCAGGTCTCAGAAAGGTGTTCGGGCTGGAG 446
QY 121 GluTyrTrpCysGlnCysValAlaAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
Db 447 GAATACTGTGTGCAGTGTGGCATGGAGCTCTCGGGCACCACCAAGAGTCAAGAGGCC 506
QY 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
Db 507 TACATCCGATAGCCAGATTTCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAAGAGGTG 566
QY 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
Db 567 TCCCTGGAGCAGGCGATCGTGTGCTGCTGCTGCCCTCCACCGGAGGCGCATCTCCAGCCGAG 626
QY 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
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Db 627 GTGGAGTGGCTCCGGAACAGGAGCCTGGTGAGCCGCTCCCTGGACCCCAATGTATACATC 686
Qy ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db 687 ACGCGGAGGACAGCCCTGGTGGTGGAGAGCCCGCTTGTGACAGGCGCAATACACC 746
Qy 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
Db 747 TGGTGGCCAAAGAACATCGTGGCAGCTCGCGCAGAGCCCTCCGCTGCTGTCATCGTCTAC 806
Qy 241 ValAsnGlyGlyTyrSerThrTyrThrGluTyrSerValCysSerAlaSerCysGlyArg 260
Db 807 GTGAACGGTGGGTGGTGGAGCTGGACCGAGTGGTCCGCTGTCAGCGCAGCTGTGGGCGC 866
Qy 261 GlyTyrGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
Db 867 GGTGGCGAAGACGGAGCCGGAGCTGCACCAACCCGGCGCTCTCAACGGGGGGCGCTTTC 926
Qy 281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
Db 927 TGTGAGGGGAGAAATGTCATACCGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 986
Qy 300 SerTyrSerProTyrSerTyrThrSerAlaCysGlyLeuAspCysThrHisTyrArgSer 319
Db 987 AGCTGGAGCCCGTGGAGCAAGTGGTGGCCCTGTGGGCTGGACTGCACCCACTGGCGGAGC 1046
Qy 320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 339
Db 1047 CGTGAGTGCTCTGACCCAGCAGCCCGCAACGGAGGGAGGAGTGGCAGGGCACTGACCTG 1106
Qy 340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
Db 1107 GACACCGCAACTGTACAGTACCTCTGTGTACACAGTCTTCTGGCCCTGAGGACGTG 1166
Qy 360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
Db 1167 GCCCTCTATGTGGGCTCATCGCGCTGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 1226
Qy 380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIle 399
Db 1227 ATCTCTGTTTATTTGCCGGAAGAGGGGCTGGACTCAGATGGCTGACTGCTGCTCAAT 1286
Qy 400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
Db 1287 CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCGCAGCAAGACAGCAACCCCATCTG 1346
Qy 420 LeuThrIleGlnProAspLeuSerThrThrThrThrThrTyrGlnGlySerLeuCysPro 439
Db 1347 CTCACCATCCAGCCGAGCTCAGC---ACCACCACTTACCCAGGGCAGTCTCTGTCTCC 1403
Qy 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeu 459
Db 1404 CGGACAGATGGGCCAGCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG 1463
Qy 460 GlyGlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
Db 1464 GGTGGCGGCCGCCACACACTGCACCAAGCTCTCCACCTCTCAGGCGGAGGATTCGTC 1523
Qy 480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
Db 1524 TCCCGGCTCTCCACCCAGAACTACTCCGCTCCGCTCCGCCGAGGCACCAAGCATGACC 1583
Qy 500 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
Db 1584 TATGGGACCTTCAACTTCTCCGGGGCGCGCTGATGATCCCTAATACAGGTATCAGCCCTC 1643
Qy 520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
Db 1644 CTATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC 1703
Qy 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
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RESULT 15

ADH71647

ID ADH71647 standard; DNA; 2881 BP.

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Qy 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
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Qy 580 GlyGluProSerProAspSerTyrSerLeuArgLeuLysLysGlnSerCysGluGlySer 599
Db 1824 GGGAGCCAGCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAGACAGTCTGTCGAGGGGCG 1883
Qy 600 TrpGlu---AspValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGln 618
Db 1884 TGGAGCAGCAGATGTGTGCACCTGGGCGAGGAGCGCCCTCCACCTCTACTACTGCGAG 1943
Qy 619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
Db 1944 CTGGAGGCCAGTGCCTGTCTACCTTCACCGACAGCTGGGCGCTTGTGCTGGTGGGA 2003
Qy 639 GluAlaLeuSerValAlaAlaAlaLysArgLeuLysLeuLeuPheAlaProValAla 658
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Qy 659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
Db 2064 TGCACCTCCTCGAGTACCAACATCCGGGTCTACTGCTGTCATGACACCCACGATGCACTC 2123
Qy 679 LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgVal 698
Db 2124 AAGGAGTGGTGCAGCTGGAGAGCAGCTGGGGGGACAGCTGATCAGGAGCCACCGGTC 2183
Qy 699 LeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSer 718
Db 2184 CTGCACCTTCAAGGACAGTTACCAACCTTGGCGCTATCCATCCACGATGTGCCAGCTCC 2243
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Db 2244 CTGTGAAGAGTAAGCTCTGTGACGTACCAAGAGATCCCTTTTATTCACATCTGGAAT 2303
Qy 739 GlyThrGluArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSer 758
Db 2304 GACACGACGGGTACTTGCACCTTCACCTGGAGCGTGTGAGCCCGCAGCATGT 2363
Qy 759 AspLeuAlaCysLysLeuTyrValTyrGlnValGluGlyAspGlyGlnSerPheSerIle 778
Db 2364 GACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGGACGGGAGAGCTTCAGCATC 2423
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Db 2424 AACTTCAACATCACCAAGGACACAAAGTGTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCG 2483
Qy 799 GlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLys 818
Db 2484 GGGGTCCCAGCCCTGGTGGGCCCCAGTGTCTTCAGATCCCTTCTCATTCGGCAGAG 2543
Qy 819 IleIleSerSerLeuAspProProCysArgArgGlyAlaAspTyrArgThrLeuAlaGln 838
Db 2544 ATAAATTCAGCTGGACCCACCTCTGTAGCGGGTGGCGAGCTGCGGAGCTCTGGCCAG 2603
Qy 839 LysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThrAlaMet 858
Db 2604 AAATCCACTGGACAGCATCTCTCAGCTTCTTTGGCTTCCAAAGCCAGCCCGCAGCCATG 2663
Qy 859 IleLeuAsnLeuTyrGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAla 878
Db 2664 ATCTCNACTGTGGAGGGCGGCGACTTCCCCACGGCAACCTCAGCCAGCTGGGTGCA 2723
Qy 879 AlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
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AC ADH71647;
 XX
 DT 25-MAR-2004 (first entry)
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 DE Human gene of the invention NOV21t SEQ ID NO:543.
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 KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003102155-A2.
 XX
 XX 11-DEC-2003.
 XX
 XX 03-JUN-2003; 2003WO-US017430.
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 PR 03-JUN-2002; 2002US-0385120P.
 PR 04-JUN-2002; 2002US-0385784P.
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 PR 18-JUN-2002; 2002US-0389884P.
 PR 19-JUN-2002; 2002US-0390006P.
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 PR 17-JUL-2002; 2002US-0396706P.
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 PR 12-AUG-2002; 2002US-0402786P.
 PR 12-AUG-2002; 2002US-0402816P.
 PR 12-AUG-2002; 2002US-0402821P.
 PR 12-AUG-2002; 2002US-0402832P.
 PR 13-AUG-2002; 2002US-0403448P.
 PR 13-AUG-2002; 2002US-0403459P.
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PR 13-AUG-2002; 2002US-0403532P.
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 PR 13-AUG-2002; 2002US-0406317P.
 PR 15-AUG-2002; 2002US-0403617P.
 PR 26-AUG-2002; 2002US-0406182P.
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 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-00423798.
 PR 12-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425453P.
 XX
 PA (CURA-) CURAGEN CORP.
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 PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ, Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K, Ettenberg S, Gangolli EA, Gerlach Vu, Goran L, Gunther E, Guo X, Gusev VV, Herrmann JU, Ji W, Kekuda R, Li L, Liu X, Macdougall JR, MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS, Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L, Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA, Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M, Zhong H;
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 WPI: 2004-081935/08.
 DR P-PSDB; ADH71648.
 XX
 PT New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 PT
 XX
 PS Example 21; SEQ ID NO 543; 1880pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and antilipemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence encodes a NOVX polypeptide of the invention.
 XX
 SQ Sequence 2881 BP; 525 A; 985 C; 869 G; 502 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.79e-298 Length: 2881
 Score: 4691.50 Matches: 887
 Percent Similarity: 98.78% Conservative: 2
 Best Local Similarity: 98.56% Mismatches: 8
 Query Match: 97.92% Indels: 3
 DB: 12 Gaps: 3
 US-10-624-932C-2 (1-898) x ADH71647 (1-2881)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAaTrpLeu 20
Db 87 ATGGCCGTCCGGCCCGGCGCTGTGGCCAGCGCTCTCTGGGCATAGTCTCTCGCGCTTGCTC 146
Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAenProValProGlyAlaAenPro 40
Db 147 CGCGGCTGGGGTGGCCAGCAGTGGCCACCGTGGCCCAACCCAGTGGCTGGCCAAACCCG 206
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTrpIleValLysAenLysPro 60
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Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 327 TGGGTGGCCAGGTGGACCACTGATCGAGCGCAGCAGACAGACGGGAGCAGTGGTGAAGCCG 386
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Db 447 GAATACTGGTGCCAGTGGCATGGAGTCTCTCGGGCACCACCAAGAGTCAGAGGCC 506
Qy 141 TyrIleArgIleAlaArgLeuArgLysAenPheGluGlnProLeuAlaLysGluVal 160
Db 507 TACATCCGCATAGCAGATTCGCGAAGAACTTCGAGCAGGAGCGCTGGCCAAAGGAGGTG 566
Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
Db 567 TCCCTGGAGCAGGAGCATGTGTGCTGCCCTGCGCTCCACGGAGGCATCCCTCCAGCCGAG 626
Qy 181 ValGluTrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIle 200
Db 627 GTGGAGTGGCTCCGGAAACGAGGACCTGGTGACCCGCTCCCTGGACCCCAATGTATACATC 686
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Db 687 ACGGGGAGACAGCCTGGTGGTGGCGACAGCGCGCTTGTGCACGGCCAACTACACC 746
Qy 221 CysValAlaLysAenIleValAlaArgArgSerAlaSerAlaValIleValTyr 240
Db 747 TGGTGGCCCAAGAACTCGTGGACGTGGCGCGCGAGCGCTCCGCTGTGTATCGTCTAC 806
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Db 807 GTGAACGGTGGTGGTGGACGTGGACCGAGTGGTGGCTGTGCAGCGCCAGCTGTGGGCGC 866
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Qy 281 CysGluGlyGlnAenVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
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Db 1107 GACACCGCAACTGTACAGTAGCTCTGTGTACACAGTGTCTTGGCCCTGAGGACGTG 1166
Qy 360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuValLeu 379

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Qy 380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAasSerSerIle 399
Db 1227 ATCTCTCGTTTATTTCCCGAAGAGAGGGGCTGAGCTCAGATGTGGCTGATCTCGTCCATT 1286
Qy 400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAasAenProHisLeu 419
Db 1287 CTACCTTCAGGCTTCAGCCCGTCAGCATCAGCCAGCAAGAGAGAGCAACCCCATCTG 1346
Qy 420 LeuThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThr 439
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Qy 480 SerArgLeuSerThrGlnAenTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
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Search completed: August 8, 2005, 05:08:55

Job time : 1765 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 8, 2005, 03:56:51 ; Search time 485 Seconds
(without alignments)
3029.642 Million cell updates/sec

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Perfect score: 4791
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Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=issued Patents NA -QWMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSELOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4638	96.8	3014	3	US-09-306-902A-1
3	2710	56.6	1787	2	US-08-808-982-2
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6	2544.5	53.1	2831	3	US-09-306-902A-3
7	2337.5	48.8	3008	4	US-09-949-016-4794
8	1895	39.6	2661	4	US-09-969-532-15
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10	1878	39.2	2703	4	US-09-969-532-11
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13	1259.5	26.3	1968	4	US-09-969-532-31
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ALIGNMENTS

RESULT 1
US-08-808-982-1
; Sequence 1, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3014 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-808-982-1

Alignment Scores:

Pred. No.: 0 Length: 3014
 Score: 4638.00 Matches: 862
 Percent Similarity: 97.88% Conservative: 17
 Best Local Similarity: 95.99% Mismatches: 19
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RESULT 2

US-09-306-902A-1

; Sequence 1, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsey

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/306,902A

FILING DATE: 07-May-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3014 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-306-902A-1

Alignment Scores:

Pred. No.:	0	Length:	3014
Score:	4638.00	Matches:	862
Percent Similarity:	97.88%	Conservative:	17
Best Local Similarity:	95.99%	Mismatches:	19
Query Match:	96.81%	Indels:	0
DB:	3	Gaps:	0

US-10-624-932C-2 (1-898) x US-09-306-902A-1 (1-3014)

Qy	1	MetAlaValArgProGlyLeuTyrProAlaLeuLeuGlyIleValLeuAlaIleTyrLeu	20
Db	1	ATGGCGCTCCGCGCGCGCTGTGGCAGTGTCTCTGGCAGTAGTCTCTCGCGCGCTGGCTT	60
Qy	21	ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro	40
Db	61	CGTGGTTCGGGTGCCAGCAGAGTGCAGGTGGCCAATCCAGTGGCGCGTGCACACCC	120
Qy	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro	60
Db	121	GACCTGCTGCCCCACTTCTGTGTAGAGCTGTAGAGCTGTACATTGTTCAGAGACACGCG	180
Qy	61	ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu	80
Db	181	GTGTTGTTGGTGTGCAAGCTGTGCTGCCACCCAGATCTTCTTCAAGTCAATGGGGAA	240
Qy	81	TyrValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro	100
Db	241	TGGTCCGCGCAGGTGATCAAGTAAATTGAACGACGACGACGACGACGACGATTTGCCA	300
Qy	101	ThrMetGluValArgIleAsnValSerArgGlnGlnValGlnLysValPheGlyLeuGlu	120
Db	301	ACCATGGAGGTCCGTATCAACGTATCGAGGACGAGCAGGTAGAGAAAGTGTGGCGTGGAG	360
Qy	121	GluTyrTyrCysGlnCysValAlaTyrPheSerSerGlyThrThrLysSerGlnLysAla	140
Db	361	GAATACCTGGTGGCAGTGTGTGGCATGGAGCTCTCTCGGGTACCAACCAAAAGTCAGAGGCC	420
Qy	141	TyrIleArgIleAlaArgLeuArgLysAsnPheGlnGlnProLeuAlaLysGluVal	160
Db	421	TACATCCGATTTGGCTATTGTGGCAAGAACTTTGAGCAGGAGCCACTTGGCCAAAGGAGTG	480
Qy	161	SerLeuGlnGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu	180
Db	481	TCACTGGAGCAAGGCATTGTACTACTTGTCCGCCCCCAGAGAGGAAATCCCCCAGCTGAG	540
Qy	181	ValGluTyrLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle	200
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGAGCCCTCCCTCGATCCCAATGTGTACATC	600

QY 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db 601 AC CGGGAGCAGACCGCTAGTCGTGCGTCAAGCCCGCTGCGCCACACGCCCACTACAC 660
QY 221 CysValAlaLysAsnIleValAlaArgArgArgSerAlaSerAlaAlaValIleValTyr 240
Db 661 TGTGTGGCCAGAACATCGTAGCCCGTGGCCGAAGCACCTCTGCAGCGGTCAATGTTTAT 720
QY 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
Db 721 GTGAACGGTGGTGGTGGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
QY 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyAlaAlaPhe 280
Db 781 GGCTGGCAGAAACGAGCGCGAGCTGCACCAACCGGCACCTCTCAACGGGGCGCTTC 840
QY 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
Db 841 TGTGAGGGGAGNATGTCCAGAAAACAGCCTGGCCCACTGTGGCCAGTGGATGGAGC 900
QY 301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
Db 901 TGGAGTTCTGGAGTAAGTGTGAGCTGTGGCTTGTGACCTGACACCCACTGGCGGAGCCGC 960
QY 321 GluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAsp 340
Db 961 GAGTGTCTGTACCCAGCACCCGCCAATGGAGGTGGAGGTGTGGGGTGTGACCTGGAC 1020
QY 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
Db 1021 ACCCGCACTGTACAGTAGACCTCTGCTGCGCACACCGCTTCTTGCCCCGAGGAGTGGCT 1080
QY 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
Db 1081 CTCTACATCGCCCTGTGCTGTGGTGTGTGCTCTCTCTGTGCTGTGGCCCTTGA 1140
QY 381 LeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeu 400
Db 1141 CTCATTACTGTGCGCAAGAGGAAGGGCTGGACTCCGATGTGGCCGACCTGCTCCATCCTC 1200
QY 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
Db 1201 ACCTCGGGCTTCAGGCTGTGACATCAAGCCAGCAAGCAGACAAACCCCACTGCTC 1260
QY 421 ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThr 440
Db 1261 ACCATCCAGCCAGACCTCAGCACCACTACCACTACCAAGGGAGTCTATGTTGAGG 1320
QY 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
Db 1321 CAGGATGGACCCAGCCCAAGTTCAGCTCTCTAATGGTCACTGTCTCAGCCCACTGGGG 1380
QY 461 GlyGlyArgHisThrLeuHisSerSerProThrSerGluAlaGluPheValSer 480
Db 1381 AGTGGCGCCATACGTTGACCAACACCTCACCACTCTGAGGCTGAGGACTTGTCTCC 1440
QY 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
Db 1441 CGCCTCTCCACCCCAAACTACTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 501 GlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu 520
Db 1501 GGGACCTTCAACTCTCTCGGGGCGCGGTGATGATCCCTAATACGGGGATCAGCTCCTC 1560
QY 521 IleProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys 540
Db 1561 ATACCCCGGATGCCATCCCGGAGAAAGATCTACGAGATCTACCTCACATGACACAG 1620
QY 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
Db 1621 CCAGAAAGCGTGAGGTGCCCCCTAGCTGGCTGTGACACCTGTGACACCTGTGCTGCTGCTGCT 1680

QY 561 CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
Db 1681 TGTGGGCCCCCAAGAGTCTCTGCTCACCCGCCAGTCACTCTTGCATAGCACCACTGTGA 1740
QY 581 GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp 600
Db 1741 GAGCCAGCCCTGACAGCTGGAGTCTGCGCTCMAAGACAGTCTCTGCGAGGGCAGTTGG 1800
QY 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
Db 1801 GAGGATGTCTGCACCTTGGTGAGGAGTCACTTCCACCTCTACTACTGCGAGCTGGAG 1860
QY 621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
Db 1861 GCCGGGGCTGTATGTCTTTCAGGAGCAGCTGGGCGCTTGGCCCTGTGTGAGAGAGGCC 1920
QY 641 LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThr 660
Db 1921 CTCAGGCTGGCTGCCACCAAGCGCTCAGGCTCTCTGTTTGTCTCCGTGGCTGTAGC 1980
QY 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 1981 TCCCTTGAACAACATCGAGTGTACTGCTTACAGCACACCCAGCGCTCTCAAGGAG 2040
QY 681 ValValGlnLeuGluLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHis 700
Db 2041 GTGGTGCACTGGAGAAGCAGCTAGTGTGACAGCTGATCCAGAGCGCTCGCGTCTGCAC 2100
QY 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db 2101 TTCMAAGCAGTTACCAACAACCTAGCTCTCTCCATCCAGACGTCGCCAGCTCCCTGTGG 2160
QY 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
Db 2161 AAGAGCAAGCTACTTGTGCTAGCTACCAAGGAGTCCCTTTTACACATCTGGAACGCGCAC 2220
QY 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
Db 2221 CAGCAGTATCTGCATCTGCACCTTACCTCTGGAGCGCATCAACGCCAGCACCGACCTG 2280
QY 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2281 GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCACTTC 2340
QY 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2341 AACATCACTAAGGACACAGGTTTGTGTAATTTGTTGGCTCTGGAGAGTGAAGGGGGTCTC 2400
QY 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
Db 2401 CCAGCCCTTGGTGGGCCCGAGTGCCTTCAAGATCCCTTCTCATTCGGCAAAAGATCATC 2460
QY 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
Db 2461 GCCAGTCTGGACCCACCTGACCGCGGGCGCGAGCTGGAGAACTCTAGCCAGAACTT 2520
QY 841 HisLeuAspSerHisLeuSerPheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2521 CACTTGGACAGCATCTTAGCTTCTTTGCTCTCAAGCCCGAGCCCTACAGCCATGATCTCTC 2580
QY 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2581 AACCTATGGAGGACGAGCACTTCCCAACGGCAACCTCGGCAGCTGCGCAGCAGCTGTG 2640
QY 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2641 GCCGAGCTGGGCCAACACAGATGCTGCTCTTTCAGGTGTGCGAGGCGCGAGGTGT 2694

RESULT 3

US-08-808-982-2
; Sequence 2, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:

Qy	343	AsnCyThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyr	362
Db	3	NACTGTACCAGTGACCTCTG-GTACACACTGCTTCGGCCCTGAGGACGTGGCCCTCTAT	61
Qy	363	valGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuVal	382
Db	62	GTGGGCGCTCATCGCGTGGCCCTGCTGCTGTGCTGTCTGTCTGTCTCATCTCGTT	121
Qy	383	TyrCysArgLysIleGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSer	402
Db	122	TATTGCCGGAAGAAGGGGGCTGGACTCAGATGGGTGACTCGTCAATTCTACCTCA	181
Qy	403	GlyPheGlnProValSerIle-LysProSerLysAlaAspAsnProHisLeuLeuThrIle	422
Db	182	GGCTTCACGCCGTCAGCATCTAAGCCACGAAAGCAGACACACCCCATCTGTCTCACCAT	241
Qy	422	eGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr	442
Db	242	CCAGCGGACCTCAGCACCAACCAACCACTTACCAGGCGAGTCTCTGTCCCCGGCAGGA	301
Qy	442	pGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGlyGlyGly	462
Db	302	TGGGGCCAGCCCCAAGTTTCAGCTCACAAATGGGCACCTGCTCAGCCGCCCTGGGTGGCGG	361


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Qy 722 rLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThrGlnAr 742
Db 1137 TAAGCTCTCTGACGTACAGGAGATCCCTTTTATCACAATCTGGAATGCGACGCG 1196
Qy 742 gTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeuAlaCy 762
Db 1197 GTACTTGCACTGCACCTTACCCCTGGAGCGGTGTGAGCCCGACGACCTAGTGACCTGGGCTG 1256
Qy 762 sLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleLeuAsnIle 782
Db 1257 CAAGCTGTGGGTGTGGCGAGTGGAGGGCGCGGAGGCTTTCAGCTCAACTTCAACAT 1316
Qy 782 eThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyValProAl 802
Db 1317 CACCAAGGACACAAGGTTTGTGAGCTGTGGCTCTGGAGAGTGAAGCGGGGTCCCGAGC 1376
Qy 802 aLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleSerSe 822
Db 1377 CCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCTCATTTGGCGAGAAGATAATTTCCAG 1436
Qy 822 rLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeuHisLe 842
Db 1437 CCTGGAGCCACCTGTAGCGGGGTGGCGACTGGCGGACTCTGGCCCCAGAACTCCACCT 1496
Qy 842 uAspSerHisLeuSerPheAlaSerLysProSerProThrAlaMetIleLeuAsnLe 862
Db 1497 GGACAGCCATCTCAGCTTCTTTGCTCCAGGCCAGCCCCACAGCCCATGATCTCAACCT 1556
Qy 862 uTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaGl 882
Db 1557 GTGGAGCGCGGCACTTCCCAACGGCAACCTCAGCGAGCTGGCTGCAGCAGTGGGTGG 1616
Qy 882 yLeuGlyGlnProAspAlaGlyLeu-PheThrVal-SerGluAlaGluCys 898
Db 1617 GACTGGCCAGCAGGCGGTGCTTCTTTTCAGTGTTCGGAGGTGAGTGC 1667
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RESULT 5

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US-08-982-3
; Sequence 3, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36, 627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-808-982-3
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Alignment Scores:

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Pred. No.: 1,46e-226 Length: 2831
Score: 2544.50 Matches: 503
Percent Similarity: 68.18% Conservative: 142
Best Local Similarity: 53.17% Mismatches: 222
Query Match: 53.11% Indels: 80
DB: 2 Gaps: 16
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US-10-624-932C-2 (1-898) x US-08-808-982-3 (1-2831)

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Qy 9 ProAlaLeuLeuGlyIleValLeuAlaAAlaTrpLeuArgGlySerGlyAlaGlnGlnSer 28
Db 61 CCAGAGCTTAGCAGGCATT-----GACTCTGTGTCAG----- 93
Qy 29 AlaThrValAlaAsnProValProGlyAlaAsnProAspLeuLeuProHisPheLeuVal 48
Db 94 ---GGACTCCAGACTCTCTCCCATCAGCACCCCGGAGCAGCTGCCTCACTTCTCTGCTG 150
Qy 49 GluProGluAspValTyrIleValLysAsnLysProValLeuLeuValCysLysAlaVal 68
Db 151 GAACAGAGGATGCTTACATCTCGTAAGAACACAGCCAGTGAATTCGACTGCCGAGCCTTC 210
Qy 69 ProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpValArgGlnValAspHisVal 88
Db 211 CCTGCCACACAGATCTACTTCAAGTGTAAATGGCGAGTGGGTAGCCAGAAAGGCCACGTC 270
Qy 89 IleGluArgSerThrAspGlySerSerGlyLeuProThrMetGluValArgIleAsnVal 108
Db 271 ACGAGAGAGAGCCTGGATGAGGCACACAGCGCTTGCATAACAGAGAGGTGCATAGAGGTG 330
Qy 109 SerArgGlnGlnValGluLysValPheGlyLeuGluGluTyrTrpCysGlnCysValAla 128
Db 331 TCGCGGAGCAGGTGGAGGAACCTTTTGGCTCAGGACTACTGGTGTAGTGTGCTGCGCC 390
Qy 129 TrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArgIleAlaArgLeuArg 148
Db 391 TGGAGCTCTTCGGGAAACCAAGAGTGCAGCGCTTACATCCGCTTGCCTACTTGGCG 450
Qy 149 LysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGluGlnGlyIleValLeu 168
Db 451 AAGAACTTTTGACGAGGAGCCTCTGGCGAAGGAGGTACCTTGGATCATGAGGTCTTCTG 510
Qy 169 ProCysArgProGluGlyIleProProAlaGluValGluTrpLeuArgAsnGluAsp 188
Db 511 CAGTGGCGCCACAGAGGAGTGCCTGTGGCTGAGGTGAATGGCTCAGAATGAAGAT 570
Qy 189 LeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSerLeuValVal 208
Db 571 GTCATGATCCCGCTCAGGACACTAATCTCTGCTCACCATTGACCACACCTCATCATC 630
Qy 209 ArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAlaLysAsnIleValAla 228
Db 631 CGCCAGCGCGGCTCTCAGACACAGCCCACTACACCTGTGTGGCAAGAAATATTGTGGCC 690
Qy 229 ArgArgArgSerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTrp 248
Db 691 AAGCGCGGAGCAGCAGCGCCACAGTCATCGTCTATGTGAACGAGAGGTGGTCAGCTGG 750
Qy 249 ThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSer 268
Db 751 GCAGATGCTCACCTGTCTTAACCCCTGCGGCGGAGGTGGCAGAAACCTACTAGGACC 810
Qy 269 CysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLys 288
Db 811 TGCACCAACCCAGCCCCCACTCAATGAGGAGTGCCTTCTCGCAGGGGACAGGGCTTGCAGAG 870
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QY 289 ThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSer 308
Db 871 ACCGCTTGCAACCAACGCTGCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGGTCC 930
QY 309 AlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArg 328
Db 931 GCCTGCAGCACAGAGTGTGGCTACTGGCGCAGCGGAGTGCATGGCACCGCGCCGCCAG 990
QY 329 AsnGlyGlyGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 348
Db 991 AACGAGGCGCTGACTGCAGCGGCGGCTACTTGACTCCAAAGAACTGCACCGATGGGCTG 1050
QY 349 CysVal-----HisSerAlaSerGlyProGlu----- 357
Db 1051 TGCCTGCTGAATCAGAGAACTTAAACGACCTTAAAGCGCGCCCTGGAGCGCTCGGGA 1110
QY 358 AspValAlaLeuTrpValGlyLeu-----IleAlaValAlaValCysLeuValLeuLeu 376
Db 1111 GACGTGGCGCTGTATCGGGGCTCTGTGGTGGCCGTCTTGTGTTCTGGCAGTTCTCATG 1170
QY 377 LeuValLeuLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAsp 396
Db 1171 GCTGTAGGAGTGTGTGTACCGGAGAACTGCGCGGACTTCGACACGGACATCACTGAC 1230
QY 397 SerSer---IleLeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAsp 415
Db 1231 TCCTCTGCTGCCCTCACTGTGTGTTTCCACCCCGTCAACTTCAAGACTCAAGCGCCAGC 1290
QY 416 AsnProHisLeuLeu-----ThrIleGlnProAspLeuSerThrThrThrThr 433
Db 1291 AACCCACAGCTCTGTACCCATCGGCCCTCCGACCTAACGCCAGTGTGTCATCTAC 1350
QY 434 GlnGlySerLeuCysProArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGly 453
Db 1351 CGCGGACCTGTGTATGCTCCCTGCAGGACTCT---GCCGACAAGATCCCTATGACTTCA 1407
QY 454 HisLeuLeuSerProLeu----- 459
Db 1408 CCCCTTCTGGATCCCTTGCCAGCCTCAAGATCAAGGTCTATGACTCCAGACCATCGGC 1467
QY 460 ---GlyGlyGly----- 462
Db 1468 TCTGGGGCTGGCTGGCTGATGAGCGGACCTGCTGGTGTCTTACCAACCCGGTACATAC 1527
QY 463 -----ArgHisThrLeuHisHisSerSerProThrSerGluAla 475
Db 1528 CCAGGCGATTTCTCCGGGACACCCACTTCTGCACCTGGCGCAGC----- 1572
QY 476 GluGluPheValSerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThr 495
Db 1573 -----GCCAGCCTTGGTTCCTCCAG---CACCTCTGCGGCCCTCCCTCGAGACCCC 1617
QY 496 SerAsnMetThrTyrGlyThrPheAsnPheLeuGlyValArgLeuMetIleProAsnThr 515
Db 1618 AGCAGCAGTGTCACTGGCACCTTTGTGCTGGTGGGAGGCTGACCATTCGCCGACA 1677
QY 516 GlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyr 535
Db 1678 GGGGTGAGCTGTGTGTACCAAAATGAGCCATTCCCGAGGCAAGTTCTATGACTTGTAT 1737
QY 536 LeuThrLeuHisLysProGluAspValArgLeuProLeuAla---GlyCysGlnThrLeu 554
Db 1738 CTACGTATCAACAAGACTGAAGACC---CTCCCACTTTCGGAAGGTTCCACAGACGTA 1794
QY 555 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 574
Db 1795 TTGAGCCCTCGGTGACTCGGGGCCACCGGGCTCTCTGCTGGCGCCCTGTGTCTTC 1854
QY 575 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGln 594
Db 1855 ACTGTGCCCACTGTGTGAAGTCAATTGCGGAGACTGGATCTTCAGCTCAAGACCCAG 1914
QY 595 SerCysGluGlySerTrpGluAspValLeuHisLeuGlyGluAlaProSerHisLeu 614

Db 1915 GCCATCAGGGCCACTGGGAGGAGGTGGTGACTTTGGATGAGGAGACTCTGAACACCCCC 1974
QY 615 TyrTyrCysGlnLeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPhe 634
Db 1975 TGCTACTGCCAGCTAGAGGCTAAATCTCCACCAATCTCTGTGGACAGCTGGGTACTAC 2034
QY 635 AlaLeuValGlyGluAlaLeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeu 654
Db 2035 GTGTTTCACGGGAGTCTTACTCCCGCTCCGAGTCAAGCGGTCCAGCTAGCATCTTC 2094
QY 655 AlaProValAlaCysThrSerLeuGluTyrAsnIleArgValTyrCysLysHisAspThr 674
Db 2095 GCCCAGCCCTCTGCACCTCCCTGGAGTATAGTCTCAGGCTTACTGTCTGGAGGACACT 2154
QY 675 HisAspAlaLeuLysGluValValGlnLeuGluLysGlnLeuGlyGlnLeuLeuGln 694
Db 2155 CTTGCAGCACTGAAGAGGTCTTAGAGCTGGAGAGGACTCTGGTGGCTACTTGGTGGAG 2214
QY 695 GluProArgValLeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAsp 714
Db 2215 GAGCCCAAGACTTGTCTTTAAGGACAGTTTACCACCACTACGCTC-TCCCTCCATGAC 2273
QY 715 ValProSerSerLeuTrpLysSerLysLeuValSerTyrGlnGluIleProPheTyr 734
Db 2274 ATCCCCCATGCCCCTGGAGGAGCAAACTACTGGCCAACTACAGGAGATTCCTCTTAC 2333
QY 735 HisIleTrpAsnGlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSer 754
Db 2334 CATGTGTGAACGGCAGCCAGAAAGCCCTGCATGCACTTTTACCCTTGGAGACATAGC 2393
QY 755 ProSerThrSerAspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGln 774
Db 2394 CTAGCTCCACTGAGTTTCACTGTAAAGTCTGCTGCGGAGGTAGAGGGGAAGGCCAG 2453
QY 775 SerPheSerIleAsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeu 794
Db 2454 ATTTTCCAGCTGCACACACCGCTGGCT---GAGACGCTGTGGCTCCCTGGATGCATC 2510
QY 795 GluSerGluAlaGlyValProAlaLeu-----ValGlyProSerAlaPheLysIlePro 812
Db 2511 TGCTCTGCCCTGGCAATCTGCCACACACAGCTGGGACCTATGCTTCAAGATACCA 2570
QY 813 PheLeuIleArgGlnLysIleIleSerSerLeuAspProProCysArgArgGlyAlaAsp 832
Db 2571 CTGTCCATCCGCCAGAAAGTCTGCAACAGCTGGACGCCCCCAACTCAGGGGCAATGAC 2630
QY 833 TrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLys 852
Db 2631 TGGCGCTCTTGGCACAGAAGCTTCTCATGGACCGGTACTGAACACTTTCGCCACCAA 2690
QY 853 ProSerProThrAlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsn 872
Db 2691 GCTAGTCCACAGCGGTGATCTTAGACCTCTGGGAAGCTCGGACAGGATGATGGGAC 2750
QY 873 LeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThr 892
Db 2751 CTCAACAGCTGGCCAGTGCCTTGGAGGAGATGGGCAAGAGTCAAGTCTGCTGATGATG 2810
QY 893 ValSerGluAlaGluCys 898
Db 2811 ACCACTGATGGCGATTGC 2828

RESULT 6
US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu

TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/306,902A
FILING DATE: 07-May-1999
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2831 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-306-902A-3

Alignment Scores:
Pred. No.: 1,46e-226 Length: 2831
Score: 2544.50 Matches: 503
Percent Similarity: 68.18% Conservative: 142
Best Local Similarity: 53.17% Mismatches: 222
Query Match: 53.11% Indels: 80
DB: 3 Gaps: 16

US-10-624-932C-2 (1-898) x US-09-306-902A-3 (1-2831)

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Qy 9 ProAlaLeuGluGlyIleValLeuAlaAThrLeuArgGlySerGlyAlaGlnSer 28
Db 61 CCGAGCTTAGCAGGCAATT-----GACTCTGGTGCCTCAG----- 93
Qy 29 AlaThrValAlaAAsnProValProGlyAlaAAsnProAspLeuLeuProHisPheLeuVal 48
Db 94 ---GGACTCCGAGCTCTCCATCATGACGCCGCGAGCAGTGCTCTCCTGCTG 150
Qy 49 GluProGluAspValTyrIleValLysAsnLysProValLeuLeuValCysLysAlaVal 68
Db 151 GAACACAGAGGATGCTACATGCTAAAGAAACAAGCAGTGAATTCGACTGCCGAGCCTC 210
Qy 69 ProAlaThrGlnLysPhePheLysCysAsnGlyGluTyrValArgGlnValAspHisVal 88
Db 211 CTTGCCACACAGATCTACTTCAAGTGTAAATGGCGAGTGGGTTAGCCAAAGGCCACGTC 270
Qy 89 IleGluArgSerThrAspGlySerSerGlyLeuLeuProThrMetGluValArgIleAsnVal 108
Db 271 ACCGAGAGAGCTGGATAGGCCACAGGCTTGGCAATACGAGAGGTGAGATAGAGGTG 330
Qy 109 SerArgGlnGlnValGluLysValPheGlyLeuGluGlyTyrTrpCysGlnCysValAla 128
Db 331 TCGCGGACAGAGTGGAGGAACCTTTTGGGCTCGAGGACTACTGGTGTCTAGTGGTGGCC 390
Qy 129 TrpSerSerSerGlyThrThrLysSerGlnLysAlaTyrIleArgIleAlaArgLeuArg 148
Db 391 TGGAGCTCTTCGGGAACCAACAGAGTCCGCGAGCTTACATCCGCAATTGCTTACTTGGCC 450
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Qy 149 LysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGluGlnGlyIleValLeu 168
Db 451 AAGAACTTTGACGAGGAGCTCTGGCGAGGAGGTACCTTGGATCATGAGGTCTTCTG 510
Qy 169 ProCysArgProProGluGlyIleProProAlaGluValGluTyrLeuArgAsnGluAsp 188
Db 511 CAGTGGCGGCCACGAGAGGAGTGCCTGTGGCTGAGTGAATGGCTCAAGATGAAGAT 570
Qy 189 LeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSerLeuValVal 208
Db 571 GTCATGATCCCTCCTCAGGACTAATCTCTCTACCATTCACCAACCTCATCATC 630
Qy 209 ArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAlaLysAsnIleValAla 228
Db 631 CGCCAGCGCGCTCTCAGACACAGCACTACACCTGTGTGCAAGAATATTTGTGGCC 690
Qy 229 ArgArgSerAlaSerAlaValIleValTyrValAsnGlyGlyTyrSerThrTrp 248
Db 691 AAGCGCGGAGCAGCAGCGCCACAGTCATGCTATGTGAACGAGGTTGGTCCAGCTGG 750
Qy 249 ThrGluTyrSerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSer 268
Db 751 GCAGAATGGTCACTCTTAACCGTGGCGCGAGTTGGCAGAAACGTACTTAGGCC 810
Qy 269 CysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLys 288
Db 811 TGCACCAACCCAGCCCACTCAATGAGGTGCTCTTCGCGAGGAGCAGGCTTGCACAG 870
Qy 289 ThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSer 308
Db 871 ACGGCTTGACCAACCGTGTGCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGGTCC 930
Qy 309 AlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArg 328
Db 931 GCCTGACGACAGAGTGGCGACTGGCGAGCGCGAGTGCATGGCAGCCGCCGCCAC 990
Qy 329 AsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 348
Db 991 AACGGAGCGCTGACTGCAGCGGAGCGCTACTTGTACTTCCAAAGAACTGCACCGATGGGCTG 1050
Qy 349 CysVal-----HisSerAlaSerGlyProGlu----- 357
Db 1051 TGGCTGCTGAATCAGAGAACTTAAACAGACCTTAAAGAGCGCCCTTGGAGCGCTCGGGA 1110
Qy 358 AspValAlaLeuTyrValGlyLeu-----IleAlaValAlaValCysLeuValLeuLeu 376
Db 1111 GAGCTGGCGCTGTATCGGGGCTCTGGTGGCGGCTCTTTGTGGTTCGGCAGTTCCTCATG 1170
Qy 377 LeuValLeuIleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAsp 396
Db 1171 GCTGTAGGAGTGTATGTTACCGGAGAACTGCGGGAGCTTCGACACGAGCATCCTGAC 1230
Qy 397 SerSer-----IleLeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAsp 415
Db 1231 TCCTCTGCTGCTCTCATCTGGTGTTCACCCCGTCAACTTCAAGACTGCAAGGCCCCAGC 1290
Qy 416 AsnProHisLeuLeu-----ThrIleGlnProAspLeuSerThrThrThrThrTyr 433
Db 1291 AACCCACAGCTCTCTGCACCCATCCGCCCTCCGAGCTTAACGCCGCTGCTGGCATCTAC 1350
Qy 434 GlnGlySerLeuCysProArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGly 453
Db 1351 CGCGGAGCTGTGTATCCCTGTCAGGACTCT--GCCGACAAGATCCCTATGACTTAATCA 1407
Qy 454 HisLeuLeuSerProLeu----- 459
Db 1408 CCCTTCTGGATCCCTTGGCCAGCTCAAGATCAAGGTCTATGATCTCAGCACCATCGGC 1467
Qy 460 ---GlyGlyGly----- 462
Db 1468 TCTGGGGCTGGCTGGCTGATGAGCGGACCTGCTGGTGTCTTACACCCGGTACATAC 1527
Qy 463 -----ArgHisThrLeuHisSerSerProThrSerGluAla 475
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Db 1528 CAGGGCGATTCTCCGGGACACCCCACTTCCTGCACCTGGCGCAGC----- 1572
Qy 476 GluGluPheValSerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThr 495
Db 1573 -----GCCAGCCTTGGTCCAG--CACCTCTGGGCTCCCTCGAGACCCC 1617
Qy 496 SerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetLeuProAsnThr 515
Db 1618 AGCAGCAGTGTCAAGTGCACCTTGGTGTGCTGGGTGGAGGCTGACCATTCCTCCGGCACA 1677
Qy 516 GlyLeuSerLeuLeuLeuProProAspAlaIleProArgGlyLysIleTyrGluIleTyr 535
Db 1678 GGGGTGAGCTGTGTGTAACAAATGGAGCCATTCCCGCAGGCAAGTCTATGACTTGTAT 1737
Qy 536 LeuThrLeuHisLysProGluAspValArgLeuProLeuAla---GlyCysGlnThrLeu 554
Db 1738 CTACGTATCAACAGACTGAAACACC--CTCCCACTTTCGGAAGGTTCACAGACAGTA 1794
Qy 555 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 574
Db 1795 TTGAGCCCTCGGTGACCTCGCGGCCACCGGGCTCTCTGTGCGCCCTGTGTGCTC 1854
Qy 575 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 594
Db 1855 ACTGTGCCCCACCTGTGTGAAGTCATTGCGGAGACTGGATCTTCAGCTCAAGACCCAG 1914
Qy 595 SerCysGluGlySerTrpGluAspValLeuHisLeuGlyGluGluAlaProSerHisLeu 614
Db 1915 GCCCATCAGGGCCACTGGGAGGAGTGGTCACTTTGGATGAGAGACTCTGAACACCCC 1974
Qy 615 TyrTyrcysGlnLeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPhe 634
Db 1975 TGCTACTGCCAGCTAGAGGTAATCTGCGACATCTGTGACCACTGCTGGTGGTGGTAC 2034
Qy 635 AlaLeuValGlyGluAlaLeuSerValAlaAlaAlaLysArgLeuLysLeuLeuPhe 654
Db 2035 GTGTTCAAGGGCGAGTCTTACTCCGCTCGCGAGTCAAGCGGCTCAGCTAGCATCTTC 2094
Qy 655 AlaProValAlaCysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThr 674
Db 2095 GCCCCAGCCCTCTGCACCTCCCTGGAGTATAGTCTCAGGGTCTACTGTCTGGAGGAC 2154
Qy 675 HisAspAlaLeuLysGluValValGlnLeuGluLysGlnLeuGlyGlnLeuIleGln 694
Db 2155 CCTGCAGCACTGAAGGAGTCTTAGAGCTCGAGGAGCTCTGGGTGGCTACTTTGGTGG 2214
Qy 695 GluProArgValLeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAsp 714
Db 2215 GAGCCCAAGACTTTGTCTTTAAGGACAGTTACCAACCTACGCTC-TCCTCCATGAC 2273
Qy 715 ValProSerSerLeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyr 734
Db 2274 ATCCCCATGCCACTGGAGGACCAAACTACTGGCCAGTACAGAGATTCCTCTTCTAC 2333
Qy 735 HisIleTrpAsnGlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSer 754
Db 2334 CATGTGTGAACGGCAGCCAGAAAGCCCTGCATCTGCATCTTACCCTCGAGACATAGC 2393
Qy 755 ProSerThrSerAspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGln 774
Db 2394 CTAGCTTCCACTGAGTTCACTGTAGGTCTGGGTGGGAGGTAGAGGGGGAAGGCCAG 2453
Qy 775 SerPheSerIleAsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeu 794
Db 2454 ATTTTCCAGCTGCACACCAACGCTGGCT--GAGACGCTCTGCTGCTCCCTGGATGCATC 2510
Qy 795 GluSerGluAlaGlyValProAlaLeu-----ValGlyProSerAlaPheLysIlePro 812
Db 2511 TGCTCTGCCCTGGCAATGTGTCACCCACACAGCTGGGACCTTATGCTTCAAGATACCA 2570
Qy 813 PheLeuIleArgGlnLysIleIleSerSerLeuAspProProCysArgArgGlyAlaAsp 832
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Db 2571 CTGTCCATCCGCCAGAGATCTGCAACAGCCCTGGAGCCGCCCAACTCACGGGCAATGAC 2630
Qy 833 TrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLys 852
Db 2631 TGGCGGCTGTGGCACAAGAGCTCTCCATGGACCGGTACTCTGAATCTACTTCGCCACCAA 2690
Qy 853 ProSerProThrAlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsn 872
Db 2691 GCTAGTCCCACAGGCGTGTATCTTAGACCTCTGGGAAGCTTCGGCAGCAGGATGATGGGAC 2750
Qy 873 LeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThr 892
Db 2751 CTCACAGCTGCGCAGTGCCTGGAGGAGATGGGCAAGTGAGATGCTGTGTAGCCATG 2810
Qy 893 ValSerGluAlaGluCys 898
Db 2811 ACCACTGATGGCGATTGC 2828

RESULT 7
US-09-949-016-4794
; Sequence 4794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4794
; LENGTH: 3008
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4794

Alignment Scores:
Pred. No.: 3,26e-207 Length: 3008
Score: 2337.50 Matches: 432
Percent Similarity: 73.77% Conservative: 136
Best Local Similarity: 56.10% Mismatches: 179
Query Match: 48.79% Indels: 23
DB: 4 Gaps: 7

US-10-624-932C-2 (1-898) x US-09-949-016-4794 (1-3008)
Qy 147 LeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGluGlnGlyIle 166
Db 9 CTACGGAGACATTTGAGCAGGAACCCCTAGGAAGAAAGTGTCTTTGGAAACAGGAAGTC 68
Qy 167 ValLeuProCysArgProGluGlyIleProProAlaGluValGluTrpLeuArgAsn 186
Db 69 TTACTCCAGTGTGCACCACTGAAGGAGTCCCAAGTGGCTGAGTGGAAATGGTTGAAAAAT 128
Qy 187 GluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSerLeu 206
Db 129 GAAGACATATTGATCCGCTGAAGATCGGAATTTTATATTACTATTGTATCAACACCTC 188
Qy 207 ValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAlaLysAsnIle 226
Db 189 ATCATTAAGCAGGCCCGACCTCTCTGTATCTGCAAAATTACACCTGTGTGCAAAACATT 248
Qy 227 ValAlaArgArgSerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSer 246
Db 249 GTTGCCCAAGGAGAAAGTCAACTGCCACTGTCTATGTCTATGTCAACGGTGGCTGGTCC 308
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; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-15

Alignment Scores:
  Pred. No.: 4,84e-166      Length: 2661
  Score: 1895.00           Matches: 383
  Percent Similarity: 58.13% Conservative: 157
  Best Local Similarity: 41.23% Mismatches: 277
  Query Match: 39.55% Indels: 112
  DB: 4 Gaps: 14

US-10-624-932C-2 (1-898) x US-09-969-532-15 (1-2661)

QY 8 TrpProAlaLeuLeuGlyIleValLeuAlaAThrLeuArgGlySer----- 23
Db 49 TGGCTCCCGTGGCTGGGG-----CTGTGCTTCTGGCGCGGACCGCGCTGCCCGA 102
QY 24 GlyAlaGlnGlnSerAlaThrValAlaAenProValProGlyAlaAenProAlaLeu 43
Db 103 GGAACGTGACAAATGGCGAAGCCCTCCCGAATCCATCCATCAGCT---CCTGGGACACTG 159
QY 44 ProHisPheLeuValGluProGluAenValTyIleValLysAenLysProValLeu 63
Db 160 CCTCATTTTCATAGAGGCGCAGATGATGCTTATATTATCATAGAGCAACCTATTGCAC 219
QY 64 ValCysLysAlaValProAlaThrGlnIlePhePheLysCysAenGlyGluTrpValArg 83
Db 220 AGGTGCAAGCGAGCGCAGCATGACATATCTTCAAAATGCAACGCGAGTGGGTCCAT 279
QY 84 GlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGlu 103
Db 280 CAGAACGAGCAGCTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGTCCGCGAA 339
QY 104 ValArgIleAenValSerArgGlnGlnValGluLysValPheGlyLeuGluTrp 123
Db 340 GTGTTTCATCAATGTTACTAGGCAACAGGTGGAGACTTCCATGGGCGCGAGCACTATTGG 399
QY 124 CysGlnCysValAlaThrSerSerGlyThrThrLysSerGlnLysAlaTyIleArg 143
Db 400 TGCACAGTGTGGCGTGGAGCCACCTGGGTACCTCCCAAGAGCAGGAAGGCTCTGTGCGC 459
QY 144 IleAlaArgLeuArgLysAenPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
Db 460 ATAGCTATTTCGGAATAACTTTGACACAGACCCACAGGAAGGAAGTTCCTCATTTGAA 519
QY 164 GlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrp 183
Db 520 GGCATGATTGTTACTGCACTGCCGCCCCACAGAGGGAGTCCCTGCTGCCGAGGTGGATGG 579
QY 184 LeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyIleThrArgGlu 203
Db 580 CTGAAAAATGAGAGGCCATTTGACTCTGAACAAGACGAGAACTATGCACACCGGGCTGAC 639
QY 204 HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyThrCysValAla 223
Db 640 CATTAACCTGATCATCAGGAGGCGCCGCTCTCGGACTCAGAAATATACACCTGCATGGCA 699
QY 224 LysAenIleValAlaArgArgSerAlaSerAlaAlaValIleValTyValAenGly 243
Db 700 GCCAACATCGTGGCTAAGAGGAGAGCCGTGTCGCCACTGTTGTGTCTACGTGGATGG 759
QY 244 GlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGln 263
Db 760 AGCTGGGAAGTGTGGAGCGCAATGTCCTGTCAGTCCA----- 798

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QY 264 LysArgSerArgSerCysThrAsnProAlaProLeuAenGlyClyAlaPheCysGluGly 283
Db 798 ----- 798
QY 284 GlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPro 303
Db 798 ----- 798
QY 304 TrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSer 323
Db 799 -----GAGTGTGAACATTTGCGGATCCGCGAGTGCA 831
QY 324 AspProAlaProArgAenGlyGlyGluCysGlnGlyThrAspLeuAspThrArgAen 343
Db 832 GCACCAACCCCGAGAAATGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAATCTGAAAAAC 891
QY 344 CysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyVal 363
Db 892 TGCACAGATGGTCTTTTGCATCTAGGCATTCAGCAATGCCAGCGACATTCGTTGTACTCG 951
QY 364 GlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuLeuValTy 383
Db 952 GGCCTTG---GGTGTCTCCGTCGTCGGCGTTCAGTCTCGTGTCTACCTGTTGTCACCTTAC 1008
QY 384 CysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSerGly 403
Db 1009 AGACGGAGCCAGAGTACTATGGCGTGGAGCTCATTTGACTCTTCTGCATTCAGAGTGGC 1068
QY 404 PheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu-----Thr 421
Db 1069 TTCCAGACCTTCAACTTCAAAACAGCTCCCTCAAGGTAACCTCCCTGCTCTGAATTCGCC 1128
QY 422 IleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThr 441
Db 1129 ATGCACCCAGATCTG---ACAGTGGACGGACATACAGCGGACCCATCTGT---CTGCAG 1182
QY 442 AspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly--- 460
Db 1183 GAC---CCTCTGGACAAAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTGTCGGAC 1239
QY 460 ----- 460
Db 1240 ATCAAAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGAGTGCTCGAGAGCTGAG 1299
QY 461 -----GlyClyArgHisThrLeuHisHis 468
Db 1300 TACCACGGCAAGAATCATTCAGGACTTTTCCCATGGAAACCAACACAGCTTTAGTACA 1359
QY 469 SerSerProThrSerGluAlaGluGluPheValSerArgLeuSerThrGlnAsnTyPhe 488
Db 1360 ATGCATCCACGAATAAATG---CCCTACATCCAAAATCTGTCA----- 1401
QY 489 ArgSerLeuProArgGlyThrSerAsnMetThrTyArgThrPheAsnPheLeuGlyGly 508
Db 1402 ---TCACTCCCAAGGACAGAACTGAGCAACAACCTGGTGTCTTTGGCCATTTAGGGGG 1458
QY 509 ArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProProAspAlaIleProArg 528
Db 1459 CGCTTAGTAGTACCAATAACAGGGGTGAGCTTACTATACCAACACGCTGCCATCCAGAG 1518
QY 529 GlyLysIleTyLeuIleTyLeuThrLeuHisLysProGluAspValArgLeuProLeu 548
Db 1519 GAGAAATCTTGGAGATTTATATGTCATCAACCAAGGTGAACCC---AGCCTCCAGTCA 1575
QY 549 AlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeu 568
Db 1576 GATGGCTCTGAGTGTCTCTGAGTCTGAAGTCACTGTGGTCTCTCCAGACATGATCGTC 1635
QY 569 ThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSer 588
Db 1636 ACCACTCCCTTTGCAATTGACATCCGCACTGTCAGATGTCTGACATCTCTGAGCATGGAAT 1695
QY 589 LeuArgLeuLysLysGlnSerCysGluGlySerTrpGluAspValLeuHisLeuGlyGlu 608

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Db 1696 ATCCATTAAAGAGAGACAGCAGCGGCAAAATGGAGGAAGTGTAGTCAGTGGAGCAT 1755
Qy 609 GluAlaProSerHisLeuTyrTyCysGlnLeuGluAlaSerAlaCysTyrValPheThr 628
Db 1756 GAATCTCATCC-----TGTTACTGCTTTTGGACCCCTTTGGCGTGCATGTGCTCTG 1809
Qy 629 GluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAlaAlaArg 648
Db 1810 GACAGCTTTGGGACCTATGCGTCACTGGAGAGCAATCACAGACTGCGCGTGAAGCAA 1869
Qy 649 LeuLysLeuLeuLeuPheAlaProValAlaCysThrSerLeuGluTyrAsnIleArgVal 668
Db 1870 CTGAAGTGGCGGTTTGGTGTGATGCTGTAACTCCCTGGATTAACAATTCAGAGTT 1929
Qy 669 TyrCysLeuHisAspThrHisAlaLeuLysGluValValGlnLeuGluLysGlnLeu 688
Db 1930 TACTGTGTGGACATACCCCTTGTGATTCCTCGAGAGTGGTTTCAGATGAAGGACATCAA 1989
Qy 689 GlyGlyGlnLeuIleGlnGluProArgValLeuHisPheLysAspSerTyrHisAsnLeu 708
Db 1990 GGTGGACAGCTCTCGAGAGAACCAAAATGCTGCAATTCAGAGGAATACCTTTAGTCTT 2049
Qy 709 ArgLeuSerIleHisAspValProSerSerLeuTyrPheLysLeuValSerTyr 728
Db 2050 CAGATTTCTGCTTGTATATTCCTCCCAATTCCTCGAGAAATTAACCATTCACCTGCCTGC 2109
Qy 729 GlnGluIleProPheTyrHisIleTyrAsnGlyThrGlnArgTyrLeuHisCysThrPhe 748
Db 2110 CAGAAGTCCCGTCTCCCGGTGTGGTGAAGTAAACCGGACCCCTGCACTGGCCCTTC 2169
Qy 749 ThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLeuTyrValTyrGln 768
Db 2170 TCCCTGGAGCGTTATACGCCCACTACCAACCCAGCTGTCTGCAAAATCTGCATTCGGCAG 2229
Qy 769 ValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLysAspThrArgPhe 788
Db 2230 CTCAAGGCCATGAACAGATCTCCAGTGCAGACATCAATCCTAGAGAGTGAACAGAA 2289
Qy 789 AlaGluLeuLeuAlaLeuGluSerGluAlaGlyValProAlaLeuValGlyProSerAla 808
Db 2290 ACCATCACTTCTTCGCACAGAGGACAGACACTTTCCTGACAGACTGGCCCCCAAGCC 2349
Qy 809 PheLysIleProPheLeuIleArgGlnLysIleSerSerLeuAspProProCysArg 828
Db 2350 TTCAAAATTCCTACTCCATCAGACAGCGGATTTGTGTACATTTGTATACCCCAATGCC 2409
Qy 829 ArgGlyAlaAspTyrArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPhe 848
Db 2410 AAAGCGAAGGACTGCGAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTAT 2469
Qy 849 PheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTyrGluAlaArgHisPhe 868
Db 2470 TTCGCTACACAAAGTAGCCCATGCTGCTCATTTGAACCTGTGGAGAGTCTGTCATCAG 2529
Qy 869 ProAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAspAla 888
Db 2530 CATGATGGTATCTTGACTCCCTGCGCTGTGCCCTTGAAGAGATTTGGAGACACACAG 2589
Qy 889 GlyLeuPheThrValSerGluAlaGlu 897
Db 2590 AAACCTCTCAACATTCAGATTCACAG 2616
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RESULT 9

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US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
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; CURRENT FILING DATE: 2001-10-02
; PRIOR FILING DATE: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-13

Alignment Scores:
Pred. No.: 3,06e-165 Length: 2694
Score: 1886.50 Matches: 384
Percent Similarity: 57.55% Conservative: 157
Best Local Similarity: 40.85% Mismatches: 276
Query Match: 39.38% Indels: 123
DB: 4 Gaps: 15
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US-10-624-932C-2 (1-898) x US-09-969-532-13 (1-2694)

Qy 8 TrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeuArgGlySer----- 23
Db 49 TGGCTCCCGTGGCTGGGG-----CTGTGCTTCTGGCGGCGGAGGACCGCGGCTGCCGA 102
Qy 24 GlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnProAspLeuLeu 43
Db 103 GGAAGTCAATGGCGAAGCCCTTCCGAAATCCATCCATCAGCT---CTGGGACACTG 159
Qy 44 ProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysProValLeuLeu 63
Db 160 CCTCATTTATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCCTATTGCACTC 219
Qy 64 ValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpValArg 83
Db 220 AGGTGCAAGCGAGCCGAGCCATGTCAGATATTTCTCAATGCAACGCGAGTGGTCCAT 279
Qy 84 GlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGlu 103
Db 280 CAGAACGACGCTCTCTGAAGAGACTCTGAGAGAGCTCAGGTTTGAAGTCCGCGAA 339
Qy 104 ValArgIleAsnValSerArgGlnValIleLysValPheGlyLeuGluGluTyrTrp 123
Db 340 GTGTTCAATCAATGTTACTAGGCAACAGTGGAGGACTTCCATGGCCGAGGACTATTGG 399
Qy 124 CysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArg 143
Db 400 TGGCAGTGTGTGGCTGGAGCCACCTGGGTACCTCCAAGAGCAGAGAGGCTCTGTGGCG 459
Qy 144 IleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
Db 460 ATAGCCTATTTCGGAATAAACTTTGAACAAGACCACCAAGAGGAGGAGTTCCCATGAA 519
Qy 164 GlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGluTrp 183
Db 520 GGCATGATTTCTACTGCACTCCGCCACAGAGGAGTCCCTGTGTCGCGAGTGGAAATGG 579
Qy 184 LeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGlu 203
Db 580 CTGAAATAATGAAGGCCCATTTGACTCTGAACAAGACGAGAAACATTTGACACCGCGCTGAC 639
Qy 204 HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 223
Db 640 CATAACTGATCATCAGGAGGACCGGCTCTCGACTCAGAAATTAACACTGATGGCA 699
Qy 224 LysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyrValAsnGly 243
Db 700 GCCAACAATCGTGGCTAAGAGAGAGAGCCCTGTCGCCCACTGTGTGGTCTACGTGATGG 759
Qy 244 GlyTyrSerThrTyrThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTyrGln 263
Db 760 AGCTGGAGAGTGTGGAGCGAATGTCGTCGTGCAAGTCCCA----- 798
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; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US 60/237,280
 ; FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11

; LENGTH: 2703
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-969-532-11

Alignment Scores:

Pred. NO.: 1.91e-164 Length: 2703
 Score: 1878.00 Matches: 383
 Percent Similarity: 57.26% Conservative: 157
 Best Local Similarity: 40.62% Mismatches: 277
 Query Match: 39.20% Indels: 126
 DB: 4 Gaps: 15

US-10-624-932C-2 (1-898) x US-09-969-532-11 (1-2703)

Qy 8 TrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeuArgGlySer----- 23
 Db TGGCTCCGGTGGCGG-----CTGGCTTGGCGGCGGAGCCGGGCTGCCGGA 102
 Qy 24 GlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnProAspLeuLeu 43
 Db 103 GGAACACTGACAAATGCGAAGCCCTCCCGAATCCATCCATCAGCT---CTTGGGACACTG 159
 Qy 44 ProHisPheLeuValGluProGluAspValTyrIleValIysAsnLysProValLeuLeu 63
 Db 160 CCTCATTTTCATAGAGGACGAGATGCTTATATTATCAAGAGCAACCCCTATTGCACTC 219
 Qy 64 ValCysIysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTyrValArg 83
 Db 220 AGTGCAGAGGAGCGGCGAGCATGCTGATATTTCTCAAAATGCAACGGCGAGTGGTCCAT 279
 Qy 84 GlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGlu 103
 Db 280 CAGAACGAGCAGCTCTCTGAAGAGACTCTGGAGAGAGCTCAGGTTTGAAGGTCGCGAA 339
 Qy 104 ValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGluTyrTrp 123
 Db 340 GTGTTTCATCAATGTTACTAGCAACAGGTGGAGACTTCCATGGGCGCGAGGACTATTGG 399
 Qy 124 CysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArg 143
 Db 400 TGCAGGTGTGGGTGGAGCCACCTGGGTACCTCCAAAGAGCAGGAAGGCTCTGTGCGC 459
 Qy 144 IleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
 Db 460 ATAGCTATTACGGAATAACTTTGAACAGACCCACAGGAGGAGTTCCCATTTGAA 519
 Qy 164 GlnGlyIleValLeuProCysArgProProGluGlyIleProAlaGluValGluTrp 183
 Db 520 GGCATGATTGTTACTGCTACGCGCCACAGAGGGAGTCTGCTGCGGAGGTGGAATGG 579
 Qy 184 LeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGlu 203
 Db 580 CTGAAAATGAAGGCCCATTTGACTCTGAACAAGACAGAGAACATTTGACACAGCGGCTGAC 639
 Qy 204 HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 223
 Db 640 CATTAACCTGATCATCAGCAGGACCGCTCTCGGACTCAGGAATAATACACTGATGGCA 699
 Qy 224 LysAsnIleValAlaArgArgSerAlaSerAlaValIleValTyrValAsnGly 243
 Db 700 GCCAACATCGTGGCTAAGAGAGAGAGGCTGTCGCGCCACTGTTGTGCTACGTGGATGG 759
 Qy 244 GlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGln 263
 Db 760 AGCTGGGAAGTGTGGAGGAATGTCCTGCTGCAAGTCCA----- 798

Qy 264 LysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGly 283
 Db 798 ----- 798
 Qy 284 GlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPro 303
 Db 798 ----- 798
 Qy 304 TrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSer 323
 Db 799 -----GAGTGTGAACATTTGGGATCCGGGATGCCACA 831
 Qy 324 AspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAspThrArgAsn 343
 Db 832 GCACCAACCCCGAGAAATCTGTGAAGTCTTAAGCCAGGAATCTGAAAAC 891
 Qy 344 CysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyrVal 363
 Db 892 TGCACAGATGCTCTTTGCATCTAGGCATTCAGAAATGCCAGCGACATTTGCTTACTCG 951
 Qy 364 GlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIleLeuValTyr 383
 Db 952 GGCTTG---GGTCTGCCGTCGTGGCGCTGTCATCTGTGTCATTCACCTTAC 1008
 Qy 384 CysArgLysLysGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSerGly 403
 Db 1009 AGACGGAGCCAGAGTGAATGCGTGGAGCTCATTGACTCTTCTGATTGACAGGTGGC 1068
 Qy 404 PheGlnProValSerIleLysProSerLysAla----- 414
 Db 1069 TTCAGACCTTCAACTTCAAAACAGTCCGTCAGGCCAAGAAATATCATGGAACATAATGATA 1128
 Qy 415 -----AspAsnProHisLeuLeu-----ThrIleGlnProAspLeuSer 427
 Db 1129 CAAGAAAAATCCTTTGGTAATCCTCTGCTCTGAAATCTGCCATGACGAGACTG--- 1185
 Qy 428 ThrThrThrThrThrGlnGlySerLeuCysProArgGlnAspGlyProSerProLys 447
 Db 1186 ACAGTGGCGGACATACACGCGGCCATCTGT---CTGCAGGAC---CTCTGGACAG 1239
 Qy 448 PheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly----- 460
 Db 1240 GAGCTCATGACAGAGCTCTCACTCTTTAAACCTTTGTGGGACATCAAAAGTGAAAGTCCAG 1299
 Qy 460 ----- 460
 Db 1300 AGCTGTTTCATGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGATCAT 1359
 Qy 461 -----GlyGlyArgHisThrLeuHisHisSerSerProThrSerGlu 474
 Db 1360 TCCAGGACTTTTCCCATGGAACACACAGCTTTAGTACAATGCAATCCAGAAATAA 1419
 Qy 475 AlaGluGluPheValSerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGly 494
 Db 1420 ATG---CCCTATACATCAAAATCTGTCA-----TCACCTCCCAACAGG 1458
 Qy 495 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 514
 Db 1459 ACAGAACTGAGGACAACTGCTGCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAAT 1518
 Qy 515 ThrGlyIleSerLeuLeuLeuProProAspAlaIleProArgGlyLysIleTyrGluIle 534
 Db 1519 ACAGGGGTGAGCTTACTATACACACGCGTGCCATCCAGAGGAGAAATCTTGGGAGATT 1578
 Qy 535 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 554
 Db 1579 TATATGTCCATCAACCAAGTGAACCC---AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 1635
 Qy 555 LeuSerProIleValSerCysGlyProGlyValLeuLeuLeuThrArgProValIleLeu 574
 Db 1636 CTGAGTCTGGAAGTACCTGTGCTCTCCAGACATGATGCTCACCACCTCCCTTTGCAATTG 1695
 Qy 575 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 594

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Db      1696  ACCATCCGCACTGTGCAAGATCTAGTTCAGCATGGAAATATCAATTTAAAGAGAGG 1755
QY      595  SerCysGluGlySerTrpGluAspValLeuHisLeuGlyGluAlaProSerHisLeu 614
Db      1756  ACACAGCAGGCAAAATGGGAGGAAGTGTGTCAGTGGAGAGATGAATCTACATCC----- 1809
QY      615  TyrTyrCysGlnLeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPhe 634
Db      1810  TGTACTGCTTTTGGACCCCTTTGGCTGTGCATGTCTCTGGACAGCTTTGGGACCTAT 1869
QY      635  AlaLeuValGlyGluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuPhe 654
Db      1870  GCCTTACTGGAGAGCAATACAGACTGTGCGGTGAGCACTGAAGGTGGCGGTTTTT 1929
QY      655  AlaProValAlaCysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThr 674
Db      1930  GGCTGCATGTCCTGTAACCTCCCTGGATTACAACCTGAGAGTTTACTGTGTGGACAATACC 1989
QY      675  HisAspAlaLeuLysGluValValGlnLeuLysGlnLeuGlyGlnLeuLysGln 694
Db      1990  CCTTGTGCACTTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCTCGAA 2049
QY      695  GluProArgValLeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAsp 714
Db      2050  GAACCAAAATGTGCAATTTCAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGAT 2109
QY      715  ValProSerSerLeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyr 734
Db      2110  ATTCCCCCACTCTCTGGAGATTAAACCAATTCACCTGCCTGCCAGGAAGTCCGTTCTCC 2169
QY      735  HisIleTrpAsnGlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSer 754
Db      2170  CGCGTGTGGTGCAGTAAACCGGACGCCCTGCACCTGTCCTCTCCCTGGAGCGTTATACG 2229
QY      755  ProSerThrSerAspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGln 774
Db      2230  CCACATACCACCCAGCTGTCTGCAAAATCTGCATTGGCGAGCTCAAGGCCATGAAACAG 2289
QY      775  SerPheSerIleAsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeu 794
Db      2290  ATCCTCCAGTGCAGACATCAATCTAGAGTGAACGAGAAACCATCACTTTCTTCGCA 2349
QY      795  GluSerGluAlaGlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeu 814
Db      2350  CAAGAGACAGCACTTTCCTCTGCACAGACTGGCCCAAAAGCCCTTCAAAATTTCCCTACTCC 2409
QY      815  IleArgGlnLysIleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArg 834
Db      2410  ATCAGACAGCGGATTTGTGTACTATTGATACCCCAANTGCCAAGGCAAGGACTGGCAG 2469
QY      835  ThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSer 854
Db      2470  ATGTTAGCACAGAAAAACACATCAACAGGAATTTATCTTATTTGCTACACAAAGTAGC 2529
QY      855  ProThrAlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSer 874
Db      2530  CCAATGCTGCTGATTTTGAACCTGTGGAGAGTGGAGTGCATCAGCATGATGTGATCTGAC 2589
QY      875  GlnLeuAlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSer 894
Db      2590  TCCCTGGCCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAACTCTCAACATTTCA 2649
QY      895  GluAlaGlu 897
Db      2650  GAATCCCAAG 2658
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RESULT 11

US-09-969-532-9

; Sequence 9, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

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; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: homo sapiens
; ORGANISM: homo sapiens
US-09-969-532-9

Alignment Scores:
Pred. No.: 1,21e-163      Length: 2736
Score: 1869.50           Matches: 384
Percent Similarity: 56.71% Conservative: 157
Best Local Similarity: 40.25% Mismatches: 276
Query Match: 39.02%      Indels: 137
DB: 4                     Gaps: 16
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US-10-624-932C-2 (1-898) x US-09-969-532-9 (1-2736)

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QY      8  TrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeuArgGlySer----- 23
Db      49  TGGCTCCCGTGGCTGGG-----CTGTGCTTCTGGCGCGAGGACCGCGGTGCCGA 102
QY      24  GlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAlaAsnProAspLeu 43
Db      103  GGAACGTACAATGGCGAAGCCCTTCCGGAATCCATCCATCAGCT---CCTGGGACACTG 159
QY      44  ProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysProValLeuLeu 63
Db      160  CCTCATTTCTAGAGGAGCCAGATGATCTATATATCAAGAGCAACCCATTGCACTC 219
QY      64  ValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpValArg 83
Db      220  AGGTGCAAGCGAGCGGCCCATGCAAGATATTCTTCANAATGCAACGCGAGTGGGTCAT 279
QY      84  GlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGlu 103
Db      280  CAGAAGCAGACAGCTCTCTGAGAGACTCTGGAGAGAGCTCAGGTTTGAAGTCCCGAA 339
QY      104  ValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGluLysTrp 123
Db      340  GTGTTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCATGGGCGCGAGGACTATTG 399
QY      124  CysGlnCysValAlaAlaTrpSerSerSerGlyThrThrLysSerGlnLysAlaTyrIleArg 143
Db      400  TGGCAGTGTGTGGCGTGGAGCCACCTGGGTACTCTCAAGAGCAAGGAAGGCTCTGTGCGC 459
QY      144  IleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
Db      460  ATAGCCTATTACGGAAAAAATTTGAACAAGACCCCAAGAGGAGGAGTCCCATTTGAA 519
QY      164  GlnGlyIleValLeuProCysArgProGluGlyIleProGluValGluTrp 183
Db      520  GGCATGATTGTACTGTCACTGCGGCCCCACAGAGGAGTCCCTGCTGCCAGGTGGAATGG 579
QY      184  LeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGlu 203
Db      580  CTGAAAAATGAAGAGCCCAITTGACTCTGAACAGAGCAGAACATTGACACCGGCTGAC 639
QY      204  HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 223
Db      640  CATAACCTGATCATCAGGAGGAGCCGCTCTCGGACTCAGGAATTTACACCTCATGGCA 699
QY      224  LysAsnIleValAlaAlaArgArgSerAlaSerAlaAlaValIleValTyrValAsnGly 243
Db      700  GCCAATCGTGGCTAAGAGGAGAGCCCTGTGCGCCACTGTTGTGCTCTACGTTGATGG 759
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; Sequence 33, Application US/09969532
; Patent No. 677232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-33

Alignment Scores:
Pred. No.: 1,78e-163 Length: 3411
Score: 1869.50 Matches: 384
Percent Similarity: 56.71% Conservative: 157
Best Local Similarity: 40.25% Mismatches: 276
Query Match: 39.02% Indels: 137
DB: 4 Gaps: 16

US-10-624-932C-2 (1-898) x US-09-969-532-33 (1-3411)

QY      8 TrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeuArgGlySer----- 23
Db      163 TGGCTCCGCGTGGGG-----CTGTGCTTCTGGCGGCAGGACCGCGGCTGCCGA 216
QY      24 GlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAlaAsnProAspLeuLeu 43
Db      217 GGAACGTGACAATGGCGAAGCCCTCCCGAATCCATCCATCAGCT---CCTGGGACACTG 273
QY      44 ProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysProValLeuLeu 63
Db      274 CCTCATTTTCATAGAGGACGAGATGATGCTATATTATATCAAGAGCAACCCCTATTGCACTC 333
QY      64 ValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTyrValArg 83
Db      334 AGGTGCAAGCGAGCGGCAGCCATCGAGATATTCTTCAATGCAACGGCGAGTGGTCCAT 393
QY      84 GlnValAspHisValIleGluArgSerThrAspGlySerGlyLeuProThrMetGlu 103
Db      394 CAGAACGAGCAGCTCTCTGAAGAGACTCTGACGAGAGCTCAGGTTTGAAGGTCGCGAA 453
QY      104 ValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGluTyrTrp 123
Db      454 GTGTTTCATCAATGTACTAGCAACAGGTGGAGGACTTCATCGGCGCCGAGGACTATTGG 513
QY      124 CysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArg 143
Db      514 TGCAGTGTGTGGGTGGAGCCACCTGGGTACTCTCAAGAGCAGGAGGCGCTCTGTGCGC 573
QY      144 IleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
Db      574 ATAGCCTATTACGGAAAACTTTGAACAAGACCCCAAGGAAGGAAGTTCCATTGAA 633
QY      164 GlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrp 183
Db      634 GGCATGATTGTACTGCACTCCGCCCCACACAGAGGAGTCCCTCTGCGCGAGGTGGAATGG 693
QY      184 LeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGlu 203
Db      694 CTGAAAAATGAGGCCATTGACTCTGAACAGACGAGAACATTGACACCGGCTGAC 753
QY      204 HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 223
Db      754 CATAACCTGATCATCAGCGAGGCAAGCGCTCTCGGACTCTCGAGAAATTACACCTGCATGGCA 813
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QY      224 LysAsnIleValAlaAlaArgArgSerAlaSerAlaAlaValIleValTyrValAsnGly 243
Db      814 GCCAACATCTGGCTAAGAGGAGAGCCCTGTCGGCCACTGTTGTGTGTACGTGGATGGG 873
QY      244 GlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGln 263
Db      874 AGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCA----- 912
QY      264 LysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGly 283
Db      912 ----- 912
QY      284 GlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPro 303
Db      912 ----- 912
QY      304 TrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSer 323
Db      913 -----GAGTGTGAACATTTGCGGATCCGGAGTGCACA 945
QY      324 AspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThrArgAsn 343
Db      946 GCACCAACCCCGAGAAATGGGGCAAAATTTCTGTGAAGGTCTAAGCCAGGAATCTGAAAAA 1005
QY      344 CysThrSerAspLeuCysVal-----HisSer 352
Db      1006 TGCACAGATGGTCTTTTGCATCTTAGATAAAAAACCTCTTCATGAATAAAAAACCCCAAGC 1065
QY      353 AlaSerGlyProGluAspValAlaLeuTyrValGlyLeuIleAlaValAlaValCysLeu 372
Db      1066 ATTGAGATGCCAGCAGACATTTGTTACTCGGGCTTG---GGTCTGCCGTCTGGGCC 1122
QY      373 ValLeuLeuLeuValLeuLeuValTyrCysArgLysLysGluGlyLeuAspSer 392
Db      1123 GTTGCACTCTGTGTCATTTGTGTGTACCTTTACAGACGGAGCCAGATGACTATGGCGTG 1182
QY      393 AspValAlaAspSerSerIleLeuThrSerGlyPheGlnProValSerIleLysProSer 412
Db      1183 GAGCTCATTTGACTTTCTGCAITGACAGGTGGCTTCAGACCTTCAACTTCAAAACAGTC 1242
QY      413 LysAla-----AspAsnProHis 418
Db      1243 CGTCAAGCCAGAAATATCATGGAACATAATGATACAGAAAAATCCTTTGTGTAACCTCG 1302
QY      419 LeuLeu-----ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThr 436
Db      1303 CTCCTGAATTTCTGCCATGCGCCAGATCTG---ACAGTGAGCCGCGACATACAGCGACCC 1359
QY      437 LeuCysProArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeu 456
Db      1360 ATCTGT---CTGAGGAC---CCTCTGGACAAGGAGCTCATGACAGTCTCCTCCTCTTT 1413
QY      457 SerProLeuGly----- 460
Db      1414 AACCTTTCTCGGACATCAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTG 1473
QY      461 -----GlyGlyArg 463
Db      1474 TCTGAGAGAGCTGAGTACCACCGCAAGAAATCATTTCCAGGACTTTTCCCTCGGAAAAAC 1533
QY      464 HisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSerArgLeuSer 483
Db      1534 CACAGCTTTAGTACAAATGTCATCCAGAAATAAAATG---CCCTACATCCAAAATCTGTCA 1590
QY      484 ThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyrGlyThrPhe 503
Db      1591 -----TCACTCCCAACAGGACAGAACTGAGGACAACTGGTGTCTTT 1632
QY      504 AsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProPro 523
Db      1633 GGCCATTTAGGGGGCGCTTAGTAATGCCAAAATACAGGGGTGAGCTTACTCATACCACAC 1692
QY      524 AspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLysProGluAsp 543
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Db 1693 GGTGCCATCCAGAGGAGAAATCTTGGGAGATTATATGTCCATCAACCAAGGTGAACCC 1752
Qy ValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyPro 563
Db 1753 ---AGCCTCCAGTCAGATGGCTCTGAGGTCTCTGAGTCTCTGAAGTCACCTGTGGTCT 1809
Qy ProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluProSer 583
Db 1810 CCAGACATGATCGTCACCACTCCCTTTGCATTGACCTCCGCGACTGTGCAGATGTCACT 1869
Qy ProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySerTrpGluAspVal 603
Db 1870 TCTGAGCATTTGCAATATCCATTTAAAGAGAGGACACAGCAGCGGCAAAATGGAGGAAGTG 1929
Qy LeuHisLeuGlyGluGluAlaProSerHisLeuTyTrpCysGlnLeuGluAlaSerAla 623
Db 1930 ATGTCAGTGAAGATGAATCATCATCC-----TGTACTGCTCTTTGGACCCCTTTGCG 1983
Qy CysTyTrpValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerVal 643
Db 1984 TGTCAATGCTCTGGACAGCTTTGGGACCTATCGCTCTACTGGAGGCCATCACAGAC 2043
Qy AlaAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThrSerLeuGlu 663
Db 2044 TGTCCCGTGAAGCAACTGAAGTGGCGGTTTTGGCTGCATGCTCTTAATCCTCGAT 2103
Qy TyrAsnIleArgValTyTrpCysLeuHisAspThrHisAspAlaLeuLysGluValValGln 683
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; Sequence 31, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 5777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: homo sapiens
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Percent Similarity: 54.85% Conservative: 128
Best Local Similarity: 36.85% Mismatches: 216
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Qy 342 ArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeu 361
Db 193 GAAAACTGCACAGATGGTCTTTGTCATCTAGGCAATGCCAGCGACATTTGCTTTG 252
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Db 253 TACTCGCGCTTG---GGTGTGCGCTGTCGCGCGCTGTCGATCTCTGGTTCATTTGTCAC 309
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Qy 833 TrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLys 852
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Search completed: August 8, 2005, 12:06:53
Job time : 579 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 8, 2005, 09:12:06 ; Search time 3771 Seconds
(without alignments)
1543.656 Million cell updates/sec

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Delop 6.0 , Delext 7.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MAXLEN=2000000000 -USER=US10624932@cgn.1.1.723 @runat_03082005_110055_3330
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4791	100.0	2752	18	US-10-624-932-1 Sequence 1, Appli
3	4698.5	98.1	2881	10	US-09-970-944-1 Sequence 15, Appli
4	4638	96.8	2697	16	US-10-240-154-15 Sequence 1, Appli
5	4638	96.8	3014	10	US-09-933-261-1 Sequence 1, Appli
6	4638	96.8	3014	14	US-10-256-702-1 Sequence 77, Appli
7	4413	92.1	3561	20	US-10-643-795A-77 Sequence 77, Appli
8	4413	92.1	3561	21	US-10-948-518-77 Sequence 13, Appli
9	4413	92.1	3580	17	US-10-311-623-13 Sequence 2, Appli
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16	2563.5	53.5	2860	17	US-10-218-779-3 Sequence 18, Appli
17	2558.5	53.4	3485	9	US-09-816-828-18 Sequence 145, App
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ALIGNMENTS

RESULT 1
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Sytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William


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; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgees, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-779-1

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Score: 4791.00 Matches: 898
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-10-624-932C-2 (1-898) x US-09-918-779-1 (1-2752)

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Qy 581 GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp 600
Db 1786 GAGCCAGCCCTGACAGCTGAGCTGCGCTCAAAAAGCAGTCTGTCGAGGGCAGCTGG 1845
Qy 601 GluAspValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
Db 1846 GAGATGTGCTGCACTTGGGCGAGGAGCGCCCTCCACCTCTACTACTGTCAGCTGGAG 1905
Qy 621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
Db 1906 GCCAGTGCCTGCTACGCTTTCACGAGCAGCTGGCGGCTTTGGCCCTGGTGGAGAGGCC 1965
Qy 641 LeuSerValAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThr 660
Db 1966 CTACGCTGGTGGCGGCGCAGCGCTCAAGCTGCTCTGTTGGCGCGGTGGCTGCACC 2025
Qy 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 2026 TCCCTCGAGTACACATCCGGGTCTACTGCGCTGATGATGATGATGATGATGATGATGAT 2085
Qy 681 ValValGlnLeuGluLysGlnLeuGlyGlnLeuLeuGlnGluProArgValLeuHis 700
Db 2086 GTGTGTGAGTGGAGAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCAGCGGTCTCTGAC 2145
Qy 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db 2146 TTCAAGGACAGTTACCAACCTCGCGCTATCCATCCACGATGTGCCAGCTCCCTGTGG 2205
Qy 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
Db 2206 AAGAGTAAGCTCTCTGTGTCAGTACACAGAGATCCCTTTTATCATCATCTGGAATGGCAGC 2265
Qy 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
Db 2266 CAGCGGTACTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2325
Qy 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2326 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGGAGAGCTTTCAGCATCAACTTC 2385
Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2386 AACATCAACCAAGGACCAAGGTTTGTGCTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2445
Qy 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
Db 2446 CCAGCCCTGTGGGGCCCCAGTGGCTTTCAGATCCCTTCTCATTCGGCAGAGATTAAT 2505
Qy 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
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Db 2506 TCCAGCTGGACCCACCTGTAGCGGGTGCACGACTGGCGGACTCTGGCCCAAGAACTC 2565
Qy 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2566 CACCTGGACAGCCATCTCAGCTTCTTTTGGCTTCCAAAGCCAGCCACAGCCATGATCTCTC 2625
Qy 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2626 AACCTGTGGAGGCGCGGCACTTCCCAACCGCAACCTCAGCCAGCTGGCTGCGAGCAGTG 2685
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2686 GCTGAGCTGGGCGCAGCAGCGCTGGCTCTTTCACAGTGTGGAGGCTGAGCTGC 2739
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RESULT 2

US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication NO. US20040096877A1

GENERAL INFORMATION:

; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsbrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glenda

; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

; FILE REFERENCES: 21402-074 US

; CURRENT APPLICATION NUMBER: US/10/624,932

; CURRENT FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: 09/918,779

; PRIOR FILING DATE: 2001-07-03

; PRIOR APPLICATION NUMBER: 60/221,409

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 60/222,840

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: 60/223,752

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,762

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,770

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,769

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/225,146

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/225,392

; PRIOR FILING DATE: 2000-08-15

; PRIOR APPLICATION NUMBER: 60/225,470

; PRIOR FILING DATE: 2000-08-15

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2752

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-624-932-1

Alignment Scores:

Pred. No.:	0	Length:	2752
Score:	4791.00	Matches:	898
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0
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Db	46	ATGGCGCTCCGGCCGGCGCTGTGGCCAGCGCTCTCTGGGCATAGTCTCGCGCGTGGCTC	105
Qy	21	ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro	40
Db	106	CGCGGCTCGGGTCCCGCAGCAGAGTGCACCGCTGGCCCAACCCAGTGCCTGGTGGCAACCCG	165
Qy	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro	60
Db	166	GACCTGCTTCCCNCTTCTGTGGAGCCCGAGATGTGTACATCGTCAAGAACAGGCCA	225
Qy	61	ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu	80
Db	226	GTGCTGCTGTGTGCAAGGCGGTGCCCGCCACGACGATCTTCTCAAGTGCACAGGGGAG	285
Qy	81	TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro	100
Db	286	TGGGTGGCCAGGTGGACACGCTGATCGAGCGAGCAGACAGCGGAGCAGTGGGCTGCC	345
Qy	101	ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu	120
Db	346	ACCATGAGGTTCGCATTATGTCTCAAGCAGCAGGTTCGAGAGGTTCGGGCTGGAG	405
Qy	121	GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla	140
Db	406	GAATACTGGTCCAGTGGCGTGGCATGTGAGTCTCTGGGGCACCAAGAGTCAAGAGGCC	465
Qy	141	TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal	160
Db	466	TACATCCGCATAGCCAGATTGCCCAAGAACTTCGAGCAGAGCGCGCTGGCCAAAGGAGTG	525
Qy	161	SerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGlu	180
Db	526	TCCTTGAGCAGGGCATCGTGTGCTGCTGCTCCAGCGAGGGCATCCCTCCAGCGGAG	585
Qy	181	ValGluTrpLeuArgAsnGluAspLeuValAspProSerSerLeuAspProAsnValTyrIle	200
Db	586	GTGGAGTGGCTCCGGAAACGAGGACCTGGTGGACCCCGTCCCTGGACCCCAATGTATACATC	645
Qy	201	ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr	220
Db	646	ACGCGGAGCACAGCTGGTGGTGGCAGAGCGCGCTTGTGTACACGCGCAACTACAC	705
Qy	221	CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr	240
Db	706	TGCGTGGCCAAAGAACATCGTGGCACGCTCGCGCAGCGCCTCCGCTGCTCATCGTCTAC	765
Qy	241	ValAsnGlyGlyTrpSerThrTrpThrTrpSerValCysSerAlaSerCysGlyArg	260
Db	766	GTGAACGGTGGGTGGTGCAGCTGGACCGAGTGGTTCGCTGTGCAGCGCCAGCTGTGGGGCGC	825
Qy	261	GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe	280
Db	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCCGCGCTCTCAACGGGGCGCTTTC	885
Qy	281	CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer	300
Db	886	TGTGAGGGGCGAGATGTCCAGAAAAACAGCCTTGGCCACCCCTGTGCCAGTAGACGGCAGC	945
Qy	301	TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg	320
Db	946	TGGAGCCCGTGGAGCAAGTGGTGGGCTGTGGGCTGGAGTGCACCCACCTGGCGGAGCCGT	1005
Qy	321	GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp	340
Db	1006	GAGTGTCTGTGACCCAGCACCCCAACGGAGGGGAGGAGTGGCCAGGGCACTGACCTGGAC	1065
Qy	341	ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla	360
Db	1066	ACCGGCACTGTACCAAGTACCTCTGTGTACACAGTGTCTTCTGGCCCTGAGGAGTGGCC	1125
Qy	361	LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle	380
Db	1126	CTCTATGTGGGCTCATCGCGGTGGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTCATC	1185
Qy	381	LeuValTyrCysArgLysGlyLeuAspSerAspValAlaAspSerSerIleLeu	400
Db	1186	CTCGTTTATTTGCCGGAAGAGGAGGGGCTGGACTCAGATGTGGCTGACTGCTCATTTCTC	1245
Qy	401	ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu	420
Db	1246	ACCTCAGGCTTCCAGGCCGTTCAGATCAAGCCCGCAAGCAGACAAACCCCATCTGCTC	1305
Qy	421	ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr	440
Db	1306	ACCATCCAGCGGACCTCAGCACCAACCCACCTACCCAGGGCAGTCTCTGTCCCGG	1365
Qy	441	GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly	460
Db	1366	CAGGATGGGCCCCAGCCCCAAGTTCCAGCTCACCAATGGGACACCTGTCTAGCCCCCTGGGT	1425
Qy	461	GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer	480
Db	1426	GGCGGGCGCCACACACTGCACACAGCTCTCCACCTCTGAGGCGCGAGGATTCGTCTCC	1485
Qy	481	ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr	500
Db	1486	CGCTCTCTCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGACCAACATGACCTAT	1545
Qy	501	GlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu	520
Db	1546	GGGACCTTCAACTTCTCTGGGGGCGGGCTGATGATCCCTAATAACAGGTATCAGCCCTCCTC	1605
Qy	521	IleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys	540
Db	1606	ATCCCCCAGATGCCATATCCCCGAGGGAGAGATCTATGAGATCTACCTCAGCTGCACAG	1665
Qy	541	ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer	560
Db	1666	CCGGAAAGAGCTGAGGTTGCCCTTAGCTGGCTGTTCAGACCTGTGTAGTCCCATCTAGT	1725
Qy	561	CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly	580
Db	1726	TGTGGACCCCTGGCGCTCTGCTCACCCGGCCAGTCACTCTGCTATGACCACTGTGGG	1785
Qy	581	GluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySerTrp	600
Db	1786	GAGCCAGCCCTGACAGCTGGAGCTTCCGCTCAAAAAGCAGTCTGTGCGAGGCGCAGCTGG	1845
Qy	601	GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu	620
Db	1846	GAGGATGTCTGCACCTGGGCGAGGAGGGCGCCCTCCACCTCTACTCTGCCAGCTGGAG	1905
Qy	621	AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla	640
Db	1906	GCAGTGGCTGTGTACGTCTTCCAGGAGAGCTGGGCGCTTTTGCCCTGTGGAGAGGCC	1965
Qy	641	LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr	660
Db	1966	CTCAGGCTGGCTGCCGCCAAGCGCTCAAGCTGCTTCTGTGTGGCGGGTGGCGCTGCACC	2025
Qy	661	SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu	680
Db	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCTGCTGATGACACCCACCATGCACTCAAGGAG	2085
Qy	681	ValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHis	700

Db 2086 GTGGTGCAGCTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCCACCGGCTCTGCAC 2145
Qy 701 PheLysAspSerTyrlHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db 2146 TTCAGGAGCATGTATCCACACCTGGCTATCCATCCACGATGTGCCAGCTCCCTGTGG 2205
Qy 721 LysSerLysLeuValSerTyrlGlnGluLeuProPheTyrlHisIleTrpAsnGlyThr 740
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Qy 741 GlnArgTyrlHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
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Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuAlaLeuGluSerGluAlaGlyVal 800
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Qy 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLysIleArgGlnLysIleIle 820
Db 2446 CCAGCCCTGGTGGGCGCCAGTGCCTTCAAGATCCCTTCTCTCATTCGCGACAGATAATT 2505
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Qy 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
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Db 2626 AACCTGTGGAGGCGCGCACTTCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2686 GCTGGAGTGGGCCAGCCAGAGCTGGCTCTTTCACAGTGTGGAGGCTGAGTGC 2739

RESULT 3

US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR FILING DATE: 60/237,862
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

Alignment Scores:

Pred. No.:	0	Length:	2881
Score:	4698.50	Matches:	888
Percent Similarity:	98.89%	Conservative:	2
Best Local Similarity:	98.67%	Mismatches:	7
Query Match:	98.07%	Indels:	3
DB:	10	Gaps:	3

US-10-624-932C-2 (1-898) x US-09-970-944-1 (1-2881)
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Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyValAsnPro 40
Db 147 CGCGGCTCGGGTGGCCAGCAGAGTGCACCGTGGCCAAACCCAGTGCCTTGTGTCACACCCG 206
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrlIleValLysAsnLysPro 60
Db 207 GACCTGCTTCCCCACTTCTTGGTGGAGCCCGGAGATGTGTACATCGTCAAGAACCAAGCCA 266
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Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrlThr 220
Db 687 ACCGCGGAGCAGCGCTGTGTGGTGGCAGACGCCCTTGTGTGACAGCGCCAACTACACC 746
Qy 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyrl 240
Db 747 TGGTGGCCCAAGAACATCGTGGCACGTCGCGCAGCGGCTCCGCTGCTGTCATCGTCTAC 806
Qy 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
Db 807 GTGAACGGTGGGTGGTGCAGCTGGACCGAGTGGTCCGCTGTCAGCGCCAGCTGTGGGCGC 866
Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
Db 867 GGTGGCAGAAACGAGCGCGGAGTGCACCAACCCGCGCTCTTCAACGGGGGCGCTTTC 926
Qy 281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
Db 927 TGTGGGGGCGAGAAATGTCCATAGCCCGCTCTCTCTCTGCTGTGCTCTGTGGAGCGC 986
Qy 300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
Db 987 AGCTGGAGCCCGTGGAGCAAGTGTGCGGCTGTGGGCTGAGTGCACCCACCTGCGCGGAGC 1046
Qy 320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeu 339
Db 1047 CGTGAGTGTCTGACCCAGCACCCCGAACGAGGGGAGGAGTGCAGGCGCACTGACCTG 1106
Qy 340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359

Db 1107 GACACCGCAACTGTACAGTGACCTCTGTGTACACAGTGTCTTGGCCCTGAGGAGCTG 1166
Qy 360 AlaleuTyrValGlyLeuIleAlaValAlaValAlaValAlaValAlaValAlaVal 379
Db 1167 GCCCTCTATGTGGGCGCTCATCGCGGTGGCGGTCTGCGCTGTCTGTCTGTCTGCTC 1226
Qy 380 IleLeuValTyrCysArgLysLysGlyLeuAspSerAspValAlaAspSerSeri 399
Db 1227 ATCTCTGTTATGCGCGAAGAGGAGGGGTGAGCTCAGATGGGTGAGCTCGTCATT 1286
Qy 400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
Db 1287 CTCACCTCAGGCTTCCAGCGCGCTCAGCATCAAGCCAGCAAGAGCAGCAACCCCATCTG 1346
Qy 420 LeuThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThr 439
Db 1347 CTCACCATCCAGCGGAGCTCAGC---ACCACCAACCACTTACCAGGGCAGCTCTGTGCC 1403
Qy 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeu 459
Db 1404 CGGAGGATGGGCCCGCCAGCCCAAGTTCCAGCTCACCNAATGGGCACCTGCTCAGCCCCCTG 1463
Qy 460 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
Db 1464 GGTGGCGCGCCACACACACTGCACACAGCTCTCCCACTCTGAGGCGGAGGAGTTCGTC 1523
Qy 480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
Db 1524 TCCGCGCTCTCCACCAAGAACTACTTCCGCTCCCTGCGCGGAGGACACAGCAACATGACC 1583
Qy 500 TyrGlyThrPheAsnLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
Db 1584 TAGGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCCCTC 1643
Qy 520 LeuIleProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
Db 1644 CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC 1703
Qy 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
Db 1704 AAGCGGAACAGCTGAGTTGCCCCCTAGCTGGCTGTGAGACCTCGCTGAGTCCCATCGTT 1763
Qy 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
Db 1764 AGCTGTGACCCCTCGCTGCTCTGCTCACCAGGCGAGTATCTGCTGATGAGCTGT 1823
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Qy 600 TrpGlu---AspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGln 618
Db 1884 TGGAGCAGGATGTGCTGCACTTGGCGAGGAGGCGCCCTCCACCTCTACTACTGCGCAG 1943
Qy 619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
Db 1944 CTGGAGCCAGTGGCTGCTAGCTTCCAGCAGAGCTGGCGCGCTTTGGCCCTGGTGGGA 2003
Qy 639 GluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAla 658
Db 2004 GAGGCCCTCAGCGTGGCTGGCGCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGTGGCC 2063
Qy 659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
Db 2064 TGCACTCTCCCTCGAGTACAACTCCGGGTCTACTTGGCTGTGATGACACCCAGATGCACTC 2123
Qy 679 LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgVal 698
Db 2124 AAGAGGTGTGAGCTGGAGAGCAGCTGGGGGAGCAGCTGATCCAGGACCCACCGGTC 2183
Qy 699 LeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSer 718
Db 2184 CTGCACCTTCAAGGACAGTTACCACTCGCGCTATCCATCCAGATGTGCCAGCTCC 2243

Qy 719 LeuTyrLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsn 738
Db 2244 CTGTGAAAGAGTAAAGTCTCTGTGACGTACCCAGGAGATCCCCCTTTATCATCTGGAAT 2303
Qy 739 GlyThrGluArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSer 758
Db 2304 GGCACGACGGGTACTTGACCTGCACCTTCACTGAGGGGTGTAGCCCCAGCACTAGT 2363
Qy 759 AspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSeri 778
Db 2364 GACCTGGCTGCAAGCTGTGGGTGTGGCAGTGGAGGGCAGCGGCAGAGCTTCAGCATC 2423
Qy 779 AsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAla 798
Db 2424 AACTTCAAGCATCACCAAGGACACCAAGTGTGGCTGTGGCTCTGGAGAGTGAAGCG 2483
Qy 799 GlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLys 818
Db 2484 GGGTCTCCAGCCCTGTGGGCCCGCAGTGTCTTCAAGATCCCTTCTCATTCGGCAGAG 2543
Qy 819 IleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGln 838
Db 2544 ATAATTTCCAGCTGCACCCACCTGTAGCGGGTGGCGACTTGGCGGACTCTGGCCAG 2603
Qy 839 LysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMet 858
Db 2604 AACTCCAGCTGGACAGCATCTCAGCTTCTTTGGCTTCAAGCCCGACCCAGCCATG 2663
Qy 859 IleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAla 878
Db 2664 ATCTCAACTGTGGAGGGCGGCACTTCCCAAGCGCACTCAGCCAGCTGGCTGCA 2723
Qy 879 AlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2724 GCAGTGGCTGAGTGGGCCAGCAGCTGGCTCTTCAAGTGTGGAGGTGAGTGC 2783

RESULT 4

US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15

Alignment Scores:
Pred. No.: 0 Length: 2697
Score: 4338.00 Matches: 862
Percent Similarity: 97.88% Conservative: 17
Best Local Similarity: 95.99% Mismatches: 19
Query Match: 96.81% Indels: 0
DB: 16 Gaps: 0

US-10-624-932C-2 (1-898) x US-10-240-154-15 (1-2697)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeu 20
Db 1 ATGGCCGTCCGGCCCGGCTGTGGCCAGTGTCTCTGGGATAGTCTCTCGCCGCTGGCTT 60

Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyValaAsnPro 40
Db |:::|
61 CGTGGTTCGGGTGCCAGCAGAGTGCACGGTGGCCAAATCCAGTGCCTGGTGGCCACACCC 120
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
Db |:::|
121 GACCTGCTGCCCCCACTTCCTGGTAGAGCTTCAGGACGCTGTACATTTGTCAAGAACAAAGCCG 180
Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db |:::|
191 GTGTGTGTGGTGGCAGGCTGTGCTGCCACCCAGATCTTCTCAAGTGCATGGGAA 240
Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db |:::|
241 TGGGTGCCCGAGGTGCATCAGTAAATGAACGACGACCGACGACGAGCGGATTGCCA 300
Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db |:::|
301 ACCATGGAGGTCCGTATCAGGTATCGAGGAGCAGAGGTAGAGAAAGTGTGGGCTGGAG 360
Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
Db |:::|
361 GAATACTGTGCGCAGTGTGGCATGGAGCTCTCGGGTACCAACAAAGTCAAGAGGCC 420
Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
Db |:::|
421 TACATCCGGATTGCTATTGGCAGAACTTTGAGCAGGAGGACCTGGCCACGAGAGTG 480
Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGlu 180
Db |:::|
481 TCACGTGAGCAAGGATTTGACTACTTGTGCGCCGCCCAAGGAATCCCCCAGCTGAG 540
Qy 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
Db |:::|
541 GTGAGTGGCTTGCAGAAATGAGACCTGTGACCCCTCCCTCGATCCCAATGTGTACATC 600
Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db |:::|
601 ACGCGGAGCACAGCTAGTGTGGTTCAGCGCCGCTGGCCGACACGCGCAACTACACC 660
Qy 221 CysValAlaLysAsnIleValAlaArgArgArgSerAlaSerAlaValIleValTyr 240
Db |:::|
661 TGTGTGGCCAAAGAACATCGTAGCCGCTGCGCGAAGACACTCTGCAGCGGTCAATGTGTTAT 720
Qy 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
Db |:::|
721 GTGAACGGTGGTGGTGCACGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 780
Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyValaPhe 280
Db |:::|
781 GGCTGGCAGAACCGAGCGGAGGTGCACCAACCGGACCTCTCAACGGGGGGCGCTTC 840
Qy 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
Db |:::|
841 TGTGAGGGGAGAAATGTCAGAAACAGCTGCGCCACTCTGTGCGCCAGTGGATGGAGC 900
Qy 301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
Db |:::|
901 TGGAGTTCGTGGAGTAAGTGTGAGCTGTGGGCTTGACTGCACCACTGGCGGAGCGCG 960
Qy 321 GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp 340
Db |:::|
961 GAGTGTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGGGGTGTGCTGACTGGAC 1020
Qy 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVala 360
Db |:::|
1021 ACCCGCAACTGTACCACTGACCTGTGCTGCACACCGCTTCTTGGCCCGAGGAGCTGGCT 1080
Qy 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
Db |:::|
1081 CTCTACATCGCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1140

Qy 381 LeuValTyrCysArgLysLysGluLysLeuAspSerAspValAlaAspSerSerIleLeu 400
Db |:::|
1141 CTCAATTTACTGTGCAAGAGGAGGCTGGACTCCGATCCGATGTGGCGAGCTCGTCCATCTCTC 1200
Qy 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
Db |:::|
1201 ACCTCGGGCTTCCAGCTGTGAGCATCAAGCCCAAGCAAGCAAGCAAGCAAGCAAGCTGTCTC 1260
Qy 421 ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThr 440
Db |:::|
1261 ACCATCCAGCCAGACCTCAGCACCACTACCACTACCACTACCACTACCACTACCACTACCACT 1320
Qy 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
Db |:::|
1321 CAGGATGGACCAAGTTCAGCTCTCTAATGGTCACTGTGTGAGGCTGAGGACTTCGTCTCC 1380
Qy 461 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer 480
Db |:::|
1381 AGTGGCGCCATACGTTGCAACCACTGCTGAGGCTGAGGACTTCGTCTCTCC 1440
Qy 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
Db |:::|
1441 CGCTCTCCACCCCAAACTACTTTCGTTCCCTGCGCCGCGGCACACGACCATGTGCTTAC 1500
Qy 501 GlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu 520
Db |:::|
1501 GGGACCTTCAACTTCTCGGGGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 521 IleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys 540
Db |:::|
1561 ATACCCCGGATGCGCATCCCGCGAGGAAGATCTACGAGATCTACCTCACACTGCACAAG 1620
Qy 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
Db |:::|
1621 CCAGAACGTGAGGTGGCCCTAGCTGGCTGTGAGACCTGCTGAGTCCAGTCTGTTAGC 1680
Qy 561 CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
Db |:::|
1681 TGTGGGCCCCCAGGAGTCTGCTCACCGGCGAGTCTCTTGCATTCGACCATGAGACCTGTGGA 1740
Qy 581 GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp 600
Db |:::|
1741 GAGCCCAAGCTGACAGTGGAGTCTGCGCTCTCAAAAGCAGTCTCTGCGAGGGCAGTTGG 1800
Qy 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrCysGlnLeuGlu 620
Db |:::|
1801 GAGATGTGTGACCTTGTGAGAGTACCTTCCACCTCTTACTACTGCGCAGCTGAG 1860
Qy 621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
Db |:::|
1861 GCCGGGCTGTCTATGCTTTCAGGAGCAGCTGGGCGCTTTGCTGCTGTTAGGAGAGGCC 1920
Qy 641 LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr 660
Db |:::|
1921 CTCAGCTGTGCTGCCACCAAGCGCTCAGGCTCTCTGTTTGTCTGCTGCTGCTGCTGCTGCT 1980
Qy 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db |:::|
1981 TCCCTTGAGTACAACTCCGAGTGTACTGCTACACACACCCACGACGCTCTCAGGAG 2040
Qy 681 ValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHis 700
Db |:::|
2041 GTGGTGCAGCTGGAGAGCAGCTAGGTGGACAGCTGATCCAGGAGCTCGCGTCTCTGCAC 2100
Qy 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db |:::|
2101 TTCAAGACAGATTACCAACCACTGCTCTCCATCCACGACGCTGCCAGCTCCCTGTGG 2160
Qy 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
Db |:::|
2161 AAGAGCAAGCTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Qy 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760

[illegible]

RESULT 5

US-09-933-261-1	
: Sequence 1, Application US/09933261	
: Publication No. US20030040046A1	
: GENERAL INFORMATION:	
: APPLICANT: Tessier-Lavigne, Marc	
: Leonardo, E. David	
: Hink, Lindsey	
: Masu, Masayuki	
: Kazuko, Keino-Masu	
: TITLE OF INVENTION: Netrin Receptors	
: NUMBER OF SEQUENCES: 8	
: CORRESPONDENCE ADDRESS:	
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP	
: STREET: 268 BUSH STREET, SUITE 3200	
: CITY: SAN FRANCISCO	
: STATE: CALIFORNIA	
: COUNTRY: USA	
: ZIP: 94104	
: COMPUTER READABLE FORM:	
: MEDIUM TYPE: Floppy disk	
: COMPUTER: IBM PC compatible	
: OPERATING SYSTEM: PC-DOS/MS-DOS	
: SOFTWARE: PatentIn Release #1.0, Version #1.30	
: CURRENT APPLICATION DATA:	
: APPLICATION NUMBER: US/09/933,261	
: FILING DATE: 20-Aug-2001	
: CLASSIFICATION: <Unknown>	
: PRIOR APPLICATION DATA:	
: APPLICATION NUMBER: 08/808,982	
: FILING DATE: <Unknown>	
: ATTORNEY/AGENT INFORMATION:	
: NAME: OSMAN, RICHARD A	
: REGISTRATION NUMBER: 36,627	
: REFERENCE/DOCKET NUMBER: UC96-217	
: TELECOMMUNICATION INFORMATION:	
: TELEPHONE: (415) 343-4341	
: TELEFAX: (415) 343-4342	
: INFORMATION FOR SEQ ID NO: 1:	
: SEQUENCE CHARACTERISTICS:	
: LENGTH: 3014 base pairs	
: TYPE: nucleic acid	

Db 841 TGTGAGGGGAGAAATGTCCAGAAACAGCCCTGCGCCACTCTGTGCCAGTGATGGGAGC 900
Qy 301 TTPSerProTTPSerLysTTPSerAlaCysGlyLeuAspCysThrHisTTPArgSerArg 320
Db 901 TGGAGTTCTGGAGTAAAGTGTGAGCTGTGGGCTTGAATCCACCACTGGCGGAGCGC 960
Qy 321 GluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAsp 340
Db 961 GAGTGTCTGTACCCAGCAGACCCCGCAATGGAGTGGAGTGTGGGGTGTGACCTGGAC 1020
Qy 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
Db 1021 ACCGCAACTGTACAGAGTACTGTGCTGCACACCGCTTCTTCCCGGAGGAGTGGCT 1080
Qy 361 LeuTyrValGlyLeuLeuAlaValAlaValCysLeuValLeuLeuValLeuLeu 380
Db 1081 CTCTACATCGGCTTGTGCTGTGGCTGTGGCTCTCTTCTGTGTGTGTGGCTTGGGA 1140
Qy 381 LeuValTyrCysArgLysLysGlyGlyLeuAspSerAspValAlaAspSerSerLeu 400
Db 1141 CTCAATTTACTGTGCAAGAGGAGGCTGGACTCCGATGTGGCGGACTGTGTCATCTC 1200
Qy 401 ThrSerGlyPheGlnProValSerLeuLysPheSerLysAlaAspAsnProHisLeuLeu 420
Db 1201 ACCTCGGGCTTCCAGCTGTGAGCATCAAGCCCAAGCAAGCAGCAACCCCCACTGCTC 1260
Qy 421 ThrLeuGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr 440
Db 1261 ACCATCCAGCCAGACCTCAGCACCACCACTACCACTACCAAGGAGTGTATGTTCAGG 1320
Qy 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
Db 1321 CAGGATGGACCCAGCCCAAGTTCCAGCTCTCTAATGTTCACTGTCTCAGCCCACTGGG 1380
Qy 461 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluPheValSer 480
Db 1381 AGTGGCCGCCATACGTTGACCAACAGCTCAGCTCAGCTCAGGCTGAGGACTTGTCTCC 1440
Qy 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
Db 1441 CGCTCTCCACCCCAAACTACTTTCTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTAC 1500
Qy 501 GlyThrPheAsnLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu 520
Db 1501 GGGACCTTCAACTTCTCGGGGCGGCTGATGATCCTTAATACGGGATCAGCCTCTC 1560
Qy 521 IleProAspAlaIleProArgGlyLysIleTyrGluLeuTyrLeuThrLeuHisLys 540
Db 1561 ATACCCCGGATGCCATCCCGGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG 1620
Qy 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
Db 1621 CCAGAACGTGAGTTGCCCCCTAGCTGGCTGTGAGACCTGCTGAGTCCAGCTGTAGC 1680
Qy 561 CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
Db 1681 TGTGGGCCCCCAGGAGTCTGCTCACCCGGCCAGTCTATCTTGAATGGACCACTGTGGA 1740
Qy 581 GluProSerProAspSerTTPSerLeuArgLeuLysGlnSerCysGlyGlySerTTP 600
Db 1741 GAGCCCAAGCCCTGACAGCTGGAGTCTGCGCTCAAAAAGCAGTCTCTCGAGGGCAGTTGG 1800
Qy 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
Db 1801 GAGGATGTCTGCACTTGTGGAGAGTACCTTCCACCTCTACTACTGCCAGCTGGAG 1860
Qy 621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
Db 1861 GCGGGGCTGTATGTCTTCCAGGAGCAGCTGGCGGCTTGTGCTGTGTGTGTGTGTGTGT 1920
Qy 641 LeuSerValAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThr 660

Db 1921 CTCAGCGTGGCTGCCCAAGCGCCTCAGCGCTCCTTCTGTTGCTCCCGTGGCTGTAGC 1980
Qy 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 1981 TCCTTGGATGTAACAATCCAGTGTACTGCTACAGACACCCACGAGCTCTCAAGAG 2040
Qy 681 ValValGlnLeuGluLysGlnLeuGlyGlnLeuLeuGlnGluProArgValLeuHis 700
Db 2041 GTGGTGAGCTGGAGAGCAGCTAGGTGGAGCAGCTGATCAGGAGCCTCGCTCTGAC 2100
Qy 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTyr 720
Db 2101 TTCAAGACAGTATACCAACCTTACGCTCTCTCCATCCAGCGTCCAGCTCCTCTGG 2160
Qy 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTTPAsnGlyThr 740
Db 2161 AAGAGCAGTACTTGTGCTACCTACGAGAGATCCCTTTTACCATCTGGACGGCACC 2220
Qy 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
Db 2221 CAGCAGTATCTGCATGCACTTCACTCGAGCGCATCAAGCGCAGCAGCAGCAGCTG 2280
Qy 761 AlaCysLysLeuTTPValTTPGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2281 GCCTGCAAGTGTGGGTGTGGCAGGTGGAGGAGATGGGAGAGTTCATTCGCAAAAGATCATC 2340
Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2341 AACATCACTAAGACACAGGTTTGTGAATTTGTGCTCTGGAGAGTGAAGGGGGGTC 2400
Qy 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIle 820
Db 2401 CCAGCCTGTGGTGGGCCAGTGTTCAGATCCCTTCTCATTCGCAAAAGATCATC 2460
Qy 821 SerSerLeuAspProProCysArgArgGlyAlaAspTTPArgThrLeuAlaGlnLysLeu 840
Db 2461 GCCAGTCTGGACCCACCTCGCAGCCGGGGCGGCGAGCTGGAGAACTCTAGCCCAAAACTT 2520
Qy 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2521 CACTGGACAGCCATCTTAGCTTCTTTCCTCCAGCCAGCCCTACAGCCATGATCTCTC 2580
Qy 861 AsnLeuTTPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2581 AACCTATGGAGGACAGGCACTTCCCAACGGCAACCTCGCCAGCTGGCAGCAGCTGTG 2640
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2641 GCGGAGCTGGGCCCAACAGATGCTGCGCTCTTCCAGGTTGCGAGGGCCGAGTGT 2694

RESULT 6

US-10-256-702-1

; Sequence 1, Application US/10256702

; Publication No. US20030059859A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/256,702

FILING DATE: 27-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/933,261

FILING DATE: 20-Aug-2001

APPLICATION NUMBER: 08/808,982

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3014 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-256-702-1

Alignment Scores:

Pred. No.:	0	Length:	3014
Score:	4638.00	Matches:	862
Percent Similarity:	97.88%	Conservative:	17
Best Local Similarity:	95.99%	Mismatches:	19
Query Match:	96.81%	Indels:	0
DB:	14	Gaps:	0

US-10-624-932C-2 (1-898) x US-10-256-702-1 (1-3014)

Qy	1	MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyLeValLeuAlaLafTrpLeu	20
Db	1	ATGGCGGTCCGGCCCGCGCTGTGGCCAGTGTCTCTGGGCATAGTCTCCGCGCTGGCTT	60
Qy	21	AtqGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro	40
Db	61	CGTGGTTCCGGTCCCGCAGAGAGTGCCAGCGTGCCCAATCCAGTCCCGGTGCAACCCC	120
Qy	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro	60
Db	121	GACCTGTGCCCCACTCTCTGGTGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAGCCG	180
Qy	61	ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu	80
Db	181	GTGTTGTGTGTGCAAGGCTGTGCTGCCACCCAGATCTCTTCAAGTGCATATGGGGAA	240
Qy	81	TrpValArgGlnValAspHisValIleGluAtqSerThrAspGlySerSerGlyLeuPro	100
Db	241	TGGGTCGCGCAGTTCGATACGTAATTGAACGACGACCCAGCAGCAGCGGATTTGCCA	300
Qy	101	ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu	120
Db	301	ACCATGGAGGTCCGTATCAAGGTATCGAGGACGAGGTAGAGAAAGTGTGGGCTGGAG	360
Qy	121	GluTyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla	140
Db	361	GAATACTGGTGCCAGTGTGTGGCATGGAGCTCTCGGGTACCACCAAAAGTCAGAAAGGC	420
Qy	141	TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal	160
Db	421	TACATCCGGATTGCCATTATTCGCALAGAACTTTTGACGAGGAGCCACTGGCCAAGGAGTG	480
Qy	161	SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu	180
Db	481	TCACTGGAGCAAGGCATTGTACTACTTGTTCGCCCCCAGAGGAATCCCCCAGCTGAG	540

Qy	181	ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle	200
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCGATCCCAATGTGTATCATC	600
Qy	201	ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr	220
Db	601	ACGCGGAGCAGAGCCTAGTGTGCTCAGGCGCCGCTGCGCCACACGCGCAACTACACC	660
Qy	221	CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr	240
Db	661	TGTGTGCCCAAGACATCGTAGCCCGTCCCGAAGCACCTCTGCAGCGGTCAATGTTTAT	720
Qy	241	ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg	260
Db	721	GTAAACGTTGGGTGGTTCGACGTGGACTGAGTGGTCTGTCAGCGCCAGCTGTGGCGGT	780
Qy	261	GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe	280
Db	781	GGCTGCGAAGAACGGAGCCGAGCTGCACCAACCCGCGACCTCTCAACGGGGCGCTTC	840
Qy	281	CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer	300
Db	841	TGTGAGGGGCGAGAAATGTCAGAAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGAGC	900
Qy	301	TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg	320
Db	901	TGGAGTTCTGTGGATAAGTGGTCAGCCTGTGGCTTGTACTGCACCCACTGGCGGAGCCGC	960
Qy	321	GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp	340
Db	961	GAGTGTCTTGACCCAGCACCCCGCAATGGAGTGGAGAGTGTGGGGTGTGACCTGGAC	1020
Qy	341	ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla	360
Db	1021	ACCGCAACTGTACAGTACCTCTGCGTCACACCGCTCTTGTGCCCCGAGGACGTGGCT	1080
Qy	361	LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle	380
Db	1081	CTCTACATCGGCTTGTGCTGTGGCTGTGCTCTCTCTGCTGTGTGGCCCTTGA	1140
Qy	381	LeuValTyrCysArgLysLysGlyLeuAspSerAspValAlaAspSerSerIleLeu	400
Db	1141	CTCATTTACTGTGCGAAGAGGAGGGCTGGACTCCGATGTGGCCGACTGTCTCCATCTTC	1200
Qy	401	ThrSerGlyPheGlnProValSerLysProSerLysAlaAspAsnProHisSerLeu	420
Db	1201	ACCTCGGCTTCCAGCTGTGACATCAAGCCAGCAAGCAGCAACCCACCTGCTC	1260
Qy	421	ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr	440
Db	1261	ACCATCCAGCCAGACCTCAGCACCCACTACACCTACAGGGCAGTCTATGTTTCGAGG	1320
Qy	441	GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly	460
Db	1321	CAGGATGGACCCAGCCCAAGTTCAGCTCTCTAATGGTCACTGTCTAGCCACCTGGGG	1380
Qy	461	GlyGlyArgHisThrIleHisSerSerProThrSerGluAlaGluGluPheValSer	480
Db	1381	AGTGGCGGCATACGTTGCACACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	481	ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr	500
Db	1441	CGCCTCTCCACCAAACTACTTTGTTCTTCCCTGCGCCCGCGGACCCAGCAACATGGCCTAC	1500
Qy	501	GlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu	520
Db	1501	GGGACCTTCACTTCTCTCGGGGCGGCTGATGATCCCTAATACGGGGATCAGCTCTCTC	1560
Qy	521	IleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys	540
Db	1561	ATACCCCGGATGCCATCCCGGAGAAAGATCTACGAGATCTACCTCACTGCAACAAG	1620
Qy	541	ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer	560

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Db 1621 CCAGAACGCTGAGGTTGCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCAGTCTGTTAGC 1680
QY CysGlyProProGlyValLeuLeuThraArgProValIleLeuAlaMetAspHisCysGly 580
Db 1681 TGTGGGCCCCAGAGTCTGCTCACCAGGCGAGTCTGCTTGGCAATGGACCACTGTGGA 1740
QY GluProSerProAspSerTrpSerLeuArgLeuLeuValysGlnSerCysGluGlySerTrp 600
Db 1741 GAGCCAGCCCTGACAGCTGGAGTCTGGCCTCAAAAAGCAGTCTCTGGAGGGGAGTTGG 1800
QY GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTrpTrpCysGlnLeuGlu 620
Db 1801 GAGGATGCTGTCACCTTGGTGGAGAGTCACTTCCCACTCTACTACTGCCAGCTGGAG 1860
QY AlaSerAlaCysTrpValPheThrGlnGlnLeuGlyArgPheAlaLeuValGlyAla 640
Db 1861 GCCGGGCGCTGTATGCTTCCAGGAGCAGCTGGCGCGCTTGGCCCTGGTAGGAGGCC 1920
QY LeuSerValAlaAlaAlaLysArgLeuLeuLeuLeuPheAlaProValAlaCysThr 660
Db 1921 CTAGCGTGGCTGCCACCAAGCGCTCAGGCTCTTCTGTTGCTCCGCTGGCTGTACG 1980
QY SerLeuGluTrpAsnIleArgValTrpCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 1981 TCCCTTGAGTACAACATCCGAGTGTACTGCTCACGACACCCACGACGCTCTCAAGGAG 2040
QY ValValGlnLeuGluLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHis 700
Db 2041 GTGGTGAGCTGGAGAGCAGCTAGGTAGTGAGCAGCTGATCCAGGAGCCTCGCTGCAC 2100
QY PheLysAspSerTrpHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db 2101 TTCAAGACAGTTACCAACCTACGCTCTCCATCCAGCAGCTGCCAGCTCCCTGTGG 2160
QY LysSerLysLeuLeuValSerTrpGlnGluIleProPheTrpHisIleTrpAsnGlyThr 740
Db 2161 AAGAGCAAGTACTTGTGACGTACAGGAGATCCCTTTTACCAATCTGGAAGCGCAC 2220
QY GlnArgTrpLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
Db 2221 CAGCAGTATCTGCACTGCACCTTCCACCTCGAGCGCATCAACGCCACACGACGACCTG 2280
QY AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2281 GCCTGCAAGGTGTGGTGTGGAGTGGAGGAGATGGGACAGCTTCAACATCACTTC 2340
QY AsnIleThrLysAspThrArgPheAlaGluLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2341 AACATCACTAAGGACACAAGGTTTGTGTAATTGTTGCTCTGGAGAGTGAAGGGGGGTC 2400
QY ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIle 820
Db 2401 CCAAGCCTGTGGGCCCGCAGTCTCAAGATCCCTTCTCATTCGGCAAAAGATCATC 2460
QY SerSerLeuAspProProCysArgArgGlyValAspTrpArgThrLeuAlaGlnLysLeu 840
Db 2461 GCCAGTCTGAGCCCAACCCTCGAGCGGGGGCGGACCTGGAGAACTCTAGCCCAAAACTT 2520
QY HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2521 CACCTGGACAGCCATCTTAGCTTCTTCCGCTCCAAAGCCAGCCCTACAGCCATGATCTC 2580
QY AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2581 AACCTATGGAGGACAGGCACTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG 2640
QY AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2641 GCCGAGTGGGCCAACAGATGCTGGCTCTTTCACGGTGTGGAGGCCGAGTGT 2694
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RESULT 7

US-10-643-795A-77

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; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-643-795A-77
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Alignment Scores:
Pred. No.: 0 Length: 3561
Score: 4413.00 Matches: 840
Percent Similarity: 93.65% Conservative: 1
Best Local Similarity: 93.54% Mismatches: 1
Query Match: 92.11% Indels: 56
DB: 20 Gaps: 1
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US-10-624-932C-2 (1-898) x US-10-643-795A-77 (1-3561)

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QY 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeu 20
Db 4 ATGGCGCTCGGCGCGGCTGTGGCAGCGCTCTGGGCATAGTCTCTCGCGCTTGGCTC 63
QY 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
Db 64 CGCGGCTCGGGTCCCGCAGCAGAGTGCCACCGTGCCCAACCCAGTGGCTGTGCCAACCCG 123
QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTrpIleValLysAsnLysPro 60
Db 124 GACCTGCTTCCCCACTCTCTGGTGGAGCCCGCAGAGTGTGTACATCTGTCAAGAACAGCCA 183
QY 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db 184 GTGCTGCTTGTGTGCAAGGCGGTGCGCCGACGACAGATCTTCTTCAAGTCAACGGGGAG 243
QY 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 244 TGGGTGCGCAGGTGGACCACTGATCGAGCGCAGCAGCAGCGGAGCAGTGGGCTGCC 303
QY 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 304 ACCATGGAGGTCCGCAATTATGTCTCAAGCAGCAGGTGCAAGAGGTGTTGGGCTGGAG 363
QY 121 GluTrpTrpCysGlnCysValAlaAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
Db 364 GAATACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 423
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141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
142 TAATCCGATAGCCATTATTGCGCAAGAACTTCGAGCAGAGCGCTGGCCAAAGAGGTG 483
161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
162 TCCCTGGAGCAGGCGATCGTGTCTGCCCTGCCCTCCACCGAGGCGATCCCTCCAGCGAG 543
181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerSerLeuAspProAsnValTyrIle 200
182 GTGAGTGGCTCCGGAACAGGAGCCTGGTGGACCCGCTCCGACCCCAATGTATACATC 603
201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
202 ACCGGGAGCAGACCTGGTGGTGGCAGACAGCGCCGCTTGTCTACACGCGCAATACAC 663
221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
222 TGGTGGCCAAAGAACATCGTGGCAGCTGCGCGCAGCGCCTCCGCTGTCTATCGTCTAC 723
241 ValAsnGlyGlyTrpSerThrTrpThrTrpGluTrpSerValCysSerAlaSerCysArg 260
723 ----- 723
261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
723 ----- 723
281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
724 -----GTGGACGGCAGC 735
301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
736 TGGAGCCGCTGGAGCAAGTGGTGGCTGTGGCTGGACTGCACCCCACTGGCGGAGCGGT 795
321 GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp 340
796 GAGTGTCTGTACCCAGACCCCGCAACGAGGGGAGGAGTGGCCAGGCGCACTGACCTGGAC 855
341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
856 ACCCGCAACTGACAGTGACCTCTGTGTACACACTGTCTTGGCCCTGAGGAGCTGGCC 915
361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
916 CTCTATGTGGGCTCATCGCGGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTCATC 975
381 LeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeu 400
976 CTCGTATTATTGCGGAAGAGGAGGGGCTGGACTCAGATGTGGCTGACTGTCCATTCTC 1035
401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
1036 ACCTCAGGCTTCCAGGCGCTCAGCATCAGCCCGAGCAGCAGCAACCCCAATCTGCTC 1095
421 ThrIleGlnProAspLeuSerThrThrThrThrThrTyrTrpGlnGlySerLeuCysProArg 440
1096 ACCATCCAGCGGACCTCAGCACCAACCCACCTACCGGGCAGTCTGTGTCCCGG 1155
441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
1156 CAGGATGGGCGCCAGCCCAAGTTCCAGCTCACCATTGGGCGACCTGTCTCAGCCCTCGGT 1215
461 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer 480
1216 GGGCGCGCCACACATGACACACAGCTCTCCCACTCTGAGCGCGAGGAGTCTGTCTCC 1275
481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
1276 CGCCTCTCCACCCAGAACTACTTCGCTCCCTCGCGGAGGCAACGACCATGACCTAT 1335

501 GlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu 520
1336 GGGACCTTCAACTTCTCGGGGGCGCTGATATCCCTAATAAGAAATCAGCCCTCTC 1395
521 IleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys 540
1396 ATCCCCCAGATGCCATACCCCGAGGGAAGATCATGAGATCTACTCTCAGCTGCACAAG 1455
541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
1456 CCGGAAGAGCTGAGGTGGCCCTTAGCTGTGTGTGAGACCTGTGAGTCCCATCGTTAGC 1515
561 CysGlyProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
1516 TGTGGACCCCTGGCGCTCTGTCTACCCGCGCAGTCACTCTGGCTATGGACCACTGTGGG 1575
581 GluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySerTrp 600
1576 GAGCCCGCCCTGACAGCTGGAGCCTGCGCCTCAAAAGCAGTCTGTGGAGGGCAGCTGG 1635
601 GluAspValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
1636 GAGGATGTGTGCACCTGGCGAGGAGGCGCCCTCCACCTCTACTACTGCGCAGCTGGAG 1695
621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyAla 640
1696 GGCAGTGCCTGTCTACCTTCCAGCAGCAGCTGGCGCGCTTGTCCCTGTGGAGAGGCC 1755
641 LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr 660
1756 CTCAGGCTGGCTGCCCGCAAGCGCTCAAGCTGTCTGTGTGGCGCGGTGGCTGCACC 1815
661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
1816 TCCTCGAGTACAACTCGGGTCTACTGCTGTCATGACACCCACCATGCACTCAAGGAG 1875
681 ValValGlnLeuLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHis 700
1876 GTGCTGACCTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCACGGGTCTGTGCAC 1935
701 PheLysAspSerTrpHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
1936 TTCAAGACAGTTACCAACCTTCCAGCTTCCATCCAGATGTGCCAGCTCCCTGTGG 1995
721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
1996 AAGAGTAAGCTCTGTCTGACTACAGGAGATCCCTTTTATCACATCTGGAAATGCGACG 2055
741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
2056 CAGCGGTACTTGGACCTGCACCTTCCCTGGAGCGTGTGAGCCCGACACTAGTGACCTG 2115
761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
2116 GCCTGCAAGCTGTGGTGTGGCAGGTGGAGGGCGACGGCAGAGCTTCAGCATCAACTTC 2175
781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
2176 AACATCACCAAGACACAAGAGTTGTCTGAGCTGTGGCTCTGGAGAGTGAAGCGGGGTC 2235
801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
2236 CCAGCCCTGTGGGCGCCAGTGCCTTCAAGATCCCTTCTCATTCGGCAGAGATAATT 2295
821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
2296 TCCAGCCTTGAGCCACCTGTAGCGGGGTGGCGACTGGCGGACTCTGGCGCAAGAACTC 2355
841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
2356 CACCTGGACAGCATCTCAGCTTCTTTGCTTCAAGCCCGAGCCCGCAGCATGATCTCTC 2415
861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880

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Db 2416 AACCTGTGGAGCGCGGCACCTTCCCAACGCGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2475
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2476 CTTGACTGGGCCAGCAGACGCTGGCCCTCTTCACAGTGTCCGAGGCTGAGTGC 2529

RESULT 8
US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-948-518-77

Alignment Scores:
Pred. No.: 0 Length: 3561
Score: 4413.00 Matches: 840
Percent Similarity: 93.65% Conservative: 1
Best Local Similarity: 93.54% Mismatches: 1
Query Match: 92.11% Indels: 56
DB: 21 Gaps: 1

US-10-624-932C-2 (1-898) x US-10-948-518-77 (1-3561)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAAlaTrpLeu 20
Db 4 ATGGCGGTCCGGCCCGCGCTGTGGCCAGCGCTCTCGGCGATAGTCTCGCGCTTGGCTC 63

Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
Db 64 CGCGGCTCGGTGCCAGCAGAGTGCACCGTGGCCCAACCCAGTGCCTGGTGCACCAACCG 123

Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValAsnLysPro 60
Db 124 GACCTGTCTCCCACTTCTCGTGGAGCCCGAGGATGTGTACATCGTCAAGAAACAAGCCA 183

Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db 184 GTGCTGTGTGTGCAAGGCCGTGCCCGCCACGCGAGATCTTCTTCAAGTGCACCGGGAG 243
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Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
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Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 304 ACCATGGAGGTCCGCATTAATGTCTCAAGGCGAGCAGGTTCGAGAAAGGTGTTCCGGGTGAG 363
Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
Db 364 GAATACTGGTCCAGTGGCATGGAGCTCTCTGGGCGACCAAGAGTCAAGAGGCC 423
Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
Db 424 TACATCCGATAGCTATTTCGCGCAAGAACTTCGAGCAGGAGCGCTGGCCCAAGAGGTG 483
Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
Db 484 TCCCTGGAGCAGGCGCATCGTCTGCTGCGCTGCGCTCACCGGAGGCGCATCCCTCCAGCCGAG 543
Qy 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
Db 544 GTGGAGTGGCTCCGGAACAGGAGCTGTGGACCCGCTCCCTGGACCCCAATGTATATCATC 603
Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db 604 ACGCGGAGCAGCACGCTGGTGGTGCAGACAGCGCGCTTGTGACACGCGCAACTACACC 663
Qy 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
Db 664 TGGGTGGCCCAAGAACTCGTGGCAGCGTGGCGCAGCGCTCCGCTGTGTCTATCTGTCTAC 723
Qy 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
Db 723 ----- 723
Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
Db 723 ----- 723
Qy 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
Db 724 -----GTGACGCGCAGC 735
Qy 301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
Db 736 TGGAGCCCGTGGAGCAAGTGGTGGCTGTGGGCTGGAGCTGCACCCACTGGCGGAGCGGT 795
Qy 321 GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp 340
Db 796 GAGTGTCTTCAGCCAGCACCCCGCAACGAGGAGGAGGAGTGCACGCGCACTGACCTGGAC 855
Qy 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
Db 856 ACCCGCAACTGTACCACTGACCTGTGTGTACACACTGCTTCTGGCCCTTGAGGAGTGGCC 915
Qy 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
Db 916 CTCTATGTGGGCTCATCGCCGTGGCGCTGTGCTGTCTGTCTGTCTGTCTGTCTCATC 975
Qy 381 LeuValTyrCysArgLysLysGluLysAspSerAspValAlaAspSerSerIleLeu 400
Db 976 CTGTTTATTTCGGAAGAGGAGGCGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC 1035
Qy 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
Db 1036 ACCTCAGGCTTCAGGCCGCTCAGCATCAGCCAGCAAGAGCAGACACCCCATCTCTCTC 1095
Qy 421 ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThr 440
Db 1096 ACCATCAGCGGAGCTCAGCACCAACCACTTACCAGGCGAGTCTCTGTGTCCCGG 1155
Qy 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
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Db 1156 CAGGATGGGCGCCAGCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCTCGGT 1215
Qy 461 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer 480
Db 1216 GCGGCGCGCCACACACTGCACCACTCTCCACCTCTCAGGCGCGAGGAGTTCTGCTCC 1275
Qy 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
Db 1276 CGCTCTCCACCCAGAACTACTTCCTCGCTCCCTGCGCGAGGCACCAAGCAATGACCTAT 1335
Qy 501 GlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu 520
Db 1336 GGGACCTTCAACTTCTTCGGGGGCGGCTGATGATCCCTAATACAGGAATCAGCCCTCTC 1395
Qy 521 IleProProAspAlaIleProArgGlyIleYrGluIleTyrLeuThrLeuHisLys 540
Db 1396 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG 1455
Qy 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
Db 1456 CCGGAAGACGTGAGTTGGCCCTAGCTGGCTGTCCAGACCCCTGCTGAGTCCCATCTGTAGC 1515
Qy 561 CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
Db 1516 TGTGGACCCCTGGCGTCTCTCACC CGGCAGTCACTCTGGCTATGGACCACTGTGGG 1575
Qy 581 GluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySerTrp 600
Db 1576 GAGCCACGCCCTGACAGCTGGAGCTCGCGCTCAAAAGAGCAGTCGTGCGAGGGCAGCTGG 1635
Qy 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
Db 1636 GAGGATGTGCTGACCTGGCGGAGGAGCGCCCTCCACCTCTACTACTGCCAGCTGGAG 1695
Qy 621 AlaSerAlaCysTrpValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
Db 1696 GCCAGTGCCTGCTACGTCTTCCAGCAGCAGCTGGCGCGCTTTCCTCTGGTGGAGAGGCC 1755
Qy 641 LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThr 660
Db 1756 CTCAGCTGGCTGCGCGCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGTGGCTGCACC 1815
Qy 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 1816 TCCTTCAGTACAACTACCCGGTCTACTGCTGCTGATGACACCCACCGATGCACCTCAAGGAG 1875
Qy 681 ValValGlnLeuGluLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHis 700
Db 1876 GTGGTGCAGCTGGGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGTCTCTGCAC 1935
Qy 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db 1936 TTCAAGGACAGTTACCAACAACCTGGCGCTATCCATCCACGATGTGCCAGCTCCCTGTGG 1995
Qy 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
Db 1996 AAGAGTAAGCTCTTGTTCAGCTACCAAGAGATCCCTTTTATCACATCTGGAAATGGCAGC 2055
Qy 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
Db 2056 CAGCGGTACTGTGACTGCACCTTCACTCCCTGAGGGGTGTCAGCCCCAGCACTAGTGACCTG 2115
Qy 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2116 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGAGCGGCAGAGCTTCACGATCAACTTC 2175
Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2176 AACATCAACCAAGGACACAAAGTTTGTCTGAGCTGTCTGCTGAGAGTGAAGCGGGGCTC 2235
Qy 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820

Db 2236 CCAGCCCTGGTGGGCCCCAGTCCTTCAAGATCCCTTCTCTCATTCGGCAGAGATAATT 2295
Qy 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
Db 2296 TCAGAGCTGGACCCACCTGTAGCGGGGTGCCGACTGGCGGACTCTGGCCCAAGAACTC 2355
Qy 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2356 CACCTGGACAGCCATCTCAGCTTCTTTGGCTTCCAAAGCCAGCCCCAGCCATGATCCTC 2415
Qy 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2416 AACCTGTGGAGCGGGGCACTTCCCAACAGCGCACTCAGCCAGCTGGCTGCAGCAGTG 2475
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2476 GCTGAGCTGGCCAGCAGCGCTGCTCTTCCAGATGTGCGAGGCTGAGTGC 2529

RESULT 9

US-10-311-623-13
; Sequence 13, Application US/10311623
; Publication No. US2004002324A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Danniell B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAPALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZO, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameen R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US2004002324A1 6052371CB1
US-10-311-623-13

Alignment Scores:
Pred. No.: 0 Length: 3580
Score: 4413.00 Matches: 840
Percent Similarity: 93.65% Conservative: 1
Best Local Similarity: 93.54% Mismatches: 1
Query Match: 92.11% Indels: 56
DB: 17 Gaps: 1

US-10-624-932C-2 (1-898) x US-10-311-623-13 (1-3580)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaIleTrpLeu 20
Db 4 ATGGCGCTCCGGCCCGCTGTGGCAGCGCTCTCTGGCATAGTCTCTCGCGCTTGGCTC 63

QY 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
DB 64 CGCGCTCGGGTGCACAGAGTGCACCGTGGCCAAACCCAGTGGCTGGTGCACACCG 123
QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
DB 124 GACCTGCTTCCCACTTCCCTGGTGGAGCCCGAGGATGTATCATCGTCAAGAACAGGCCA 183
QY 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
DB 184 GTGCTGCTTGTGTGACAGCCGCTGCCCGCAGCAGATCTTCTTCAAGTGCAACGGGAG 243
QY 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
DB 244 TGGGTGGCCAGGTGGACACGATGATCGAGCGCAGCAGACAGCGGAGCAGTGGGCTGCC 303
QY 101 ThrMetGluValArgIleAsnValSerArgGlnValGluLysValPheGlyLeuGlu 120
DB 304 ACCATGGAGGTCCGATTAATGTCTCAAGGCAGCAGGTTCGAGAGGTGTTCGGGCTGGAG 363
QY 121 GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
DB 364 GAATACTGGTGCCAGTGGTGGATGGAGCTCTCGGGCACCACCAAGAGTCAAGAGGCC 423
QY 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
DB 424 TACATCCGATAGCTTATTTCCGCAAGAACTTCGAGCAGGAGCGCTGGCCCAAGAGGTG 483
QY 161 SerLeuGlnGlnIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
DB 484 TCCCTGGAGCAGGGCATCGTCTCCCTGCGCTCCACCGGAGGGCATCCCTCCACGCGGAG 543
QY 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
DB 544 GTGGAGTGGCTCCCGACAGGAGACTGGTGACCCGCTCCCTGGACCCCAATGTATATCATC 603
QY 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
DB 604 ACGGGGAGCAGACGCTGGTGGTGGCAGCAGCGCCGCTTGTGACAGCGCCCAACTACACC 663
QY 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
DB 664 TGCCTGGCCCAAGAACATCGTGGCAGCGTGGCGCAGCGCTCCGCTGCTGTATCGTCTAC 723
QY 241 ValAsnGlyGlyTyrTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
DB 723 ----- 723
QY 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
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QY 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
DB 724 -----GTGGACGGCAGC 735
QY 301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
DB 736 TGGAGCCCGTGGACCAAGTGTGGCTGGTGGCTGGACTGCACCCACTGGCGGAGCCGT 795
QY 321 GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp 340
DB 796 GAGTGTCTGACCCAGCAGCCCGCAACAGGAGGGGAGGAGTGGCAGGGCACTGACCTGGAC 855
QY 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
DB 856 ACCCGCAACTGTACAGTACCTCTGTGTACACACTGCTTCTGGCCCTGAGGACGCTGGCC 915
QY 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValIle 380
DB 916 CTCTATGTGGCCCTCATCGCGGTGGCGTCTGGCTGGTCTGGCTGGCTGGCTGGCTGGCT 975
QY 381 LeuValTyrCysArgLysLysGluLysLeuAspSerAspValAlaAspSerSerIleLeu 400

DB 976 CTGCTTTATTTCGCGGAAGAGGAGGGCTGGACTCAGATGTGGCTGACTCGTCCATCTCTC 1035
QY 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
DB 1036 ACCTCAGGCTTCCAGCCCGTCAAGATCAAGCCCAAGCAGCAACACCCCATCTGTCTC 1095
QY 421 ThrIleGlnProAspLeuSerThrThrThrThrTyrTyrGlnGlySerLeuCysProArg 440
DB 1096 ACCATCCAGCGGAGCTTCAAGCACCAACCAACCACTTACAGGGCAGTCTCTGTGCCCGG 1155
QY 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
DB 1156 CAGGATGGCGCCAGCCCAAGTTCCAGCTCACCATAATGGSCACCTGCTCAGCCCCCTGGGT 1215
QY 461 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer 480
DB 1216 GCGGGCGCCACACACTGCACCAAGCTCTCCACCTCTGAGGCGGAGGATTCGTCTCC 1275
QY 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
DB 1276 CGCTCTCCACCCAGAACTACTTCCGCTCCCTGCGCCGAGGACACAGCAATGACCTAT 1335
QY 501 GlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu 520
DB 1336 GSGACCTTCAACTTCTCGGGGCGCGCTCATGTATCCCTAATACAGGAATCAGCTCTCTC 1395
QY 521 IleProAspAlaIleProArgGlyValIleTyrGluIleTyrLeuThrLeuHisLys 540
DB 1396 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAG 1455
QY 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
DB 1456 CCGAGACGCTGAGGTGGCCCTAGCTGGCTGTGAGACCTCTGAGTCCCATCGTTAGC 1515
QY 561 CysGlyProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
DB 1516 TGTGGACCCCTGGCTGCTGCTCACCAGCGCAGTCTATCTGGCTATGGACCATGTGGG 1575
QY 581 GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp 600
DB 1576 GAGCCCGACGCTGACAGCTGGAGCTTGGCTGTCAAAAGCAGTCTGTCGAGGGCAGCTGG 1635
QY 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
DB 1636 GAGATGTGCTGCACCTGGGCGAGGAGCGCCCTCCACCTCTACTACTCCAGCTGGAG 1695
QY 621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
DB 1696 GCCAGTGGCTGTACGCTTTCACCGAGCAGCTGGGCGGCTTTGGCCCTGGTGGAGAGGCC 1755
QY 641 LeuSerValAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr 660
DB 1756 CTGAGGTGGCTGCGCCCAAGCGCTCAAGCTGCTTGTGTGGCGCGTGGCTGCACC 1815
QY 661 SerLeuLysThrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
DB 1816 TCCCTCGAGTACAACTCCGGGTCTACTGCTCGATGACACCCACCATGCACTCAAGAG 1875
QY 681 ValValGlnLeuGlyLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHis 700
DB 1876 GTGGTGCAGCTGGAGAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCACGGTCTCTGCAC 1935
QY 701 PheLysAspSerThrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
DB 1936 TTCAAGCAGAGTTACCAACACCTGCGCTATCCATCCAGATGTGCCAGCTCCCTGTGG 1995
QY 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
DB 1996 AAGAGTAAGCTCTTGTGAGTACCAAGAGATCCCTTTTATCACATCTCGAATGGCAGC 2055
QY 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760

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Db 2056 CAGCGGTACTTGCACTTCCACCTTCCACCTGGAGCGTGTGAGCCCGACACCTAGTGACCTG 2115
Qy 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2116 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC 2175
Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2176 AACATCACCAGGACACAAGGTTTGTGAGCTGTGGCTCTGGAGAGTGAAGCGGGGTG 2235
Qy 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
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Qy 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2356 CACCTGGACAGCCATCTCAGCTTCTTTGCTTCCAAAGCCCGACCCACAGCCATGATCCCT 2415
Qy 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2416 AACCTGTGGAGGCGGGCACTTCCCAACGGCACTCAGCCAGCTGGCTGCAGCAGTG 2475
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2476 GCTGGAGTGGCCAGCAGACGCTGGCTCTTCCACAGTGTGGAGGCTGAGTGC 2529

RESULT 10
US-09-933-261-2
; Sequence 2, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1787 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-933-261-2
Alignment Scores:
Pred. No.: 3 61e-276 Length: 1787
Score: 2710.00 Matches: 544
Percent Similarity: 97.50% Conservative: 1
Best Local Similarity: 97.32% Mismatches: 11
Query Match: 56.56% Indels: 9
DB: 10 Gaps: 0
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Qy 363 ValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuVal 382
Db 62 GTGGGCTCATCGCCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
Qy 383 TyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSer 402
Db 122 TATTGCCGAAGAGAGAGGGCTGGACTCAGATGTGGCTGACTCGTCCATCTCACCCTCA 181
Qy 403 GlyPheGlnProValSerIle-LysProSerLysAlaAspAsnProHisLeuLeuThrI 422
Db 182 GGCTTCCAGCCGTCAGCATCTAAGCCAGCAAGCAGACAACCCCATCTGCTCACCAT 241
Qy 422 eGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThrThr 442
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Qy 442 pGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGlyGlyG 462
Db 302 TGGGCCCGACCCCAAGTTCAGCTCACCATATGGGCACCTGCTCAGCCCTCTGGGTGGCG 361
Qy 462 yArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSerArgLe 482
Db 362 CCGCCACACACTGCACACACAGCTCTCCACCTCTGAGGGCGAGAGTTCGTCTCCCGCCT 421
Qy 482 uSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyrGlyTh 502
Db 422 CTCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGACACAGCAACATGACCTATGGAC 481
Qy 502 rPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIlePr 522
Db 482 CTTCAACTTCTCGGGGGCGGCTGATGATCCCTATACAGGAATCAGCCTCTCATCCC 541
Qy 522 oProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLysProGl 542
Db 542 CCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACTCAGCTGCACAAAGCCGGA 601
Qy 542 uAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGl 562
Db 602 AGACGTGAGGTGGCCCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
Qy 562 yProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluPr 582
Db 662 ACCCCCTGGGCTCTGCTCACC CGGCAGTCTATCTGGCTATGACCACTGTGGGAGCC 721
Qy 582 oSerProAspSerTrpSerLeuArgIleLysLysGlnSerCysGluGlySerTrpGluAs 602
Db 722 CAGCCCTGACAGCTGGAGCGCTGGCCCTCAAAAAAGCAGTCTGTGCGAGGAGC-TGGGAGGA 780
Qy 602 pValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSe 622
Db 781 TGT-CTGCACTGGGCGAGAGGGCCCTCCCACTCTACTCTGCTGCTGCTGCTGCTGCTG 839
Qy 622 rAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSe 642
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QY 502 rPheAsnLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIlePr 522
DB 482 CTTCAACTTCCTCGGGGCGCGGTGATGCCCTAATACAGGAATCAGCCCTCTCATCCC 541
QY 522 oProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLysProG1 542
DB 542 CCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAAGCGGA 601
QY 542 uAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuLeuSerProIleValSerCysG1 562
DB 602 AGAGCTGAGGTTCCTAGCTGGCTGTGCAGACCTGTGAGTCCCATCTGTTAGCTGTGG 661
QY 562 yProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluPr 582
DB 662 ACCCTCTGGCGTCTCTACCCGCGCAGATCATCTGGCTATGGACCATGTGGGAGGCC 721
QY 582 oSerProAspSerTyrSerLeuArgLeuLysGlnSerCysGluGlySerTyrGluAs 602
DB 722 CAGCCCTGACAGCTGGAGCTTGGCCCTCAAAAGACAGTGTGTGGAGGAGC-TGGGAGGA 780
QY 602 pValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSe 622
DB 781 TGT-CTGCACCTGGCGAGGAGCGCCCTCCACCTCTACTACTGCGAGCTGGAGGCCAG 839
QY 622 rAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSe 642
DB 840 TGCCTGCTAGCTTTCAACGAGAGCTGGGCCCTTTGGCCCTGGTGGGAGAGCCCTCAG 899
QY 642 rValAlaAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThrSerLe 662
DB 900 CGTGGCTGCCGCCNAGCGCTCAAGCTGCTTCTGTGTGGCCGCTGGCCCTGCACCTCCCT 959
QY 662 uGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValVa 682
DB 960 CGAGTACAACTCCGGGTCTACTGCTCATGCATGCACCCAGATGCCTCAAGGAGGTGT 1019
QY 682 lGlnLeuGluLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHisPheLys 702
DB 1020 GCAGCTGGAGAGGAGCTGGGGGAGACAGTGTCCAGAGGCCACGGGTCTCTGCACCT-AA 1078
QY 702 sAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTyrLysSe 722
DB 1079 GGACAGTTACCAACACTGCC-CTATC-ATCCAGATGTGCCAGCTCCCTGTGGAGAG 1136
QY 722 rLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTyrAsnGlyThrGlnAr 742
DB 1137 TAAGCTCCTTGTAGCTTACCAGGAGATCCCTTTTATCATCTGGAATGGCAGCGAGCG 1196
QY 742 gTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAsnLeuAlaCy 762
DB 1197 GTACTTGCATGACCTTCACTCCCTGGAGCGTGTGAGCCCGACACTAGTACCTTGGCGCTG 1256
QY 762 sLysLeuTyrValTyrGlnValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnI1 782
DB 1257 CAGCTGTGGGTGTGGAGGTGGAGGGCGAGCGGAGAGCTTCAGCATCACTTCAACAT 1316
QY 782 eThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyValProAl 802
DB 1317 CACCAAGGACACAGGTTTCTCAGCTGTGGCTCTGGAGTGAAGCGGGGTGCCAGC 1376
QY 802 aLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleSerSe 822
DB 1377 CTGGGTGGGCCCCAGTGCCCTTCAAGATCCCCCTTCTCATTCGGGAGAGATAATTTCCAG 1436
QY 822 rLeuAspProProCysArgArgGlyAlaAspTyrArgThrLeuAlaGlnLysLeuHisLe 842
DB 1437 CCTGGACCCACCTGTAGGCGGGGTGCCGACTGGCGAGCTCTGGCCAGAACTCCACCT 1496
QY 842 uAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLe 862
DB 1497 GGACAGCATCTCAGCTTCTTGGCTCTCAAGCCGAGCCCGACAGCCATGATCTCAACCT 1556
QY 862 uTyrGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaG1 882

DB 1557 GTGGGAGGCGCGGCACCTTCCCAACGGCAACCTCAGCAGCTGCTGCAGCACTGGCTGG 1616
QY 882 yLeuGlyGlnProAspAlaGlyLeu-PheThrVal-SerGluAlaGluCys 898
DB 1617 GACTGGCCAGCAGGACGGTGGCTTCTTTCACAGTGTTCGAGGCTGAGTGC 1667
RESULT 12
US-10-764-420-2213
; Sequence 2213, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Ian, Yejun
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; TITLE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2213
; LENGTH: 3866
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-2213
Alignment Scores:
Pred. No.: 4,32e-261 Length: 3866
Score: 2572.50 Matches: 505
Percent Similarity: 68.80% Conservative: 150
Best Local Similarity: 53.05% Mismatches: 236
Query Match: 53.69% Indels: 61
DB: 21 Gaps: 15
US-10-624-932C-2 (1-898) x US-10-764-420-2213 (1-3866)
QY 1 MetAlaValArgProGlyLeuTyrProAlaLeuLeuGlyIleValLeuAlaLaTyr--- 19
DB 417 ATGAGGCGCGGAGCGGGGTGGGAGCGCGCTCTCTGCGCGCTGTCTTCTTCTGGGAT 476
QY 20 -----LeuArgGly-----SerGlyAlaGlnGlnSerAlaThrValAlaAsn 33
DB 477 CCGACACCGAGCCTAGCAGCGTGTGACTCTGTCTGGCCAG-----GTGCTCCCAGAC 527
QY 34 ProValProGlyAlaAsnProAspLeuLeuProHisPheLeuValGluProGluAspVal 53
DB 528 TCCTACCCATCAGCCCTCGGAGCAGCTGCGCTACTTCTTATTTGGGCCACAGGACGCC 587
QY 54 TyrIleValIysAsnLysProValLeuLeuValCysLysAlaValProAlaThrGlnIle 73
DB 588 TACATCGTAAAGAACCAAGCCAGTGGAACTGCACCTGCAGAGCCTTCCTCTGCCACGAGATC 647
QY 74 PhePheLysCysAsnGlyGluTyrValArgGlnValAspHisValIleGluArgSerThr 93
DB 648 TACTTCAAGTGTAAATGGCAGTGGGTGAGCCAGCAATGACCACGCTCACACAGGAGGCTG 707
QY 94 AspGlySerSerGlyLeuProThrMetGluValArgIleAsnValSerArgGlnGlnVal 113
DB 708 GATGAGGCCACAGCCTTGGCGGTGCGAGAGGTGCAGATCAGGTGTACCGGCAGCAAGTG 767
QY 114 GluLysValPheGlyLeuGluTyrTyrCysGlnCysValAlaTyrSerSerSerGly 133
DB 768 GAGAAACTCTTCGGCTTCAGGACTACTGTGTGCAGTGTGTGCGCTTGGAGCTCTTCGGGA 827
QY 134 ThrThrLysSerGlnLysAlaTyrIleArgIleAlaArgLeuArgLysAsnPheGluGln 153
DB 828 ACTACCAAGAGTCGCGGACCTACATCCGCGATTCGCTTACTTTCGCAAGAACTTTTGACG 887

Qy 154 GluProLeuAlaLysGluValSerLeuGluGlnGlnIleValLeuProCysArgPro 173
| | | | | : : : : :
Db 888 GAGCCTCTGGCCAGGAGTACCTTGGATCATGAGTCTCTGCGAGTGGCGCCACCG 947
Qy 174 GluGlyIleProProAlaGluValGluTrpLeuArgAsnGluAaspLeuValAaspProSer 193
| | | | | : : : : :
Db 948 GAGGAGTGGCTGTGGCTGAGTGAATGGCTCAAGATGAAGATGTCATTGACCCGCT 1007
Qy 194 LeuAaspProAenValTyrIleThrArgGluHisSerLeuValValArgGlnAlaArgLeu 213
| | | | | : : : : :
Db 1008 CAGGACATACTCTCTCCTCACCATTGACCACACCTCATCTCCGCGCCGCGCGCTC 1067
Qy 214 AlaAaspThrAlaAsnTyrThrCysValAlaLysAsnIleValAlaArgArgSerAla 233
| | | | | : : : : :
Db 1068 TCAGACGCGCCACTACACTGTGTGGCCAGGATATCGTGGCCAGGCGCGGAGCACC 1127
Qy 234 SerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpGluTrpSerVal 253
| | | | | : : : : :
Db 1128 CGCGCCACAGTCATCGTCTATGTGAATGGAGCTGGTCCAGTGGCGAGAGTGGTCAACC 1187
Qy 254 CysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsnProAla 273
| | | | | : : : : :
Db 1188 TGTTCCAATCGCTGTGGCCGAGGCTGGCAGAGGCTACTCGGACCTGCACCAATCCAGCC 1247
Qy 274 ProLeuAenGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCysAlaThr 293
| | | | | : : : : :
Db 1248 CCACTCAATGAGGCGCTCTCTGTGAGGACAGGCCCTTCAGAGACAGCTTGCACACC 1307
Qy 294 LeuCysProValAaspGlySerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAasp 313
| | | | | : : : : :
Db 1308 GTGTGCCAGTGGATGAGCGGTGACCGGAGTGGAGCAAGTGGTCTGCGCTGCAGCACAG 1367
Qy 314 CysThrHisTrpArgSerArgGluCysSerAaspProAlaProArgAsnGlyGlyGluGlu 333
| | | | | : : : : :
Db 1368 TGTGCGCACTGGCGAGCGCGAGTGCATGCGACCGCCACCGCCAGAGCGGCGGTGAC 1427
Qy 334 CysGlnGlyThrAaspLeuAaspThrArgAsnCysThrSerAaspLeuCysVal----- 350
| | | | | : : : : :
Db 1428 TGCAGCGGAGCGTACTTGCATCCAGNACTGCATGATGGGCTGTGGTGTCTGAATCAG 1487
Qy 351 -----HisSerAlaSerGlyProGluAaspValAlaLeuTyr 362
| | | | | : : : : :
Db 1488 AGAACTCTAAACGACCCCTAAAGCCACCCCTGGAGACATCGGAGATGTGGCACTGTAC 1547
Qy 363 ValGlyLeu-----IleAlaValAlaValCysLeuValLeuLeuLeuValLeuLeu 381
| | | | | : : : : :
Db 1548 GCAGGCTTGTGGTGGCGCTCTTGTGGTGTAGCGGTTCTCATGGCGGAGGAGTATC 1607
Qy 382 ValTyrCysArgLysGlyLeuAaspSerAaspValAlaAaspSerSer-----IleLeu 400
| | | | | : : : : :
Db 1608 GTATACCGGAGAACTGCGGGACTTCGACACGAGCATCACCGACTCTCTGCGGCGCTC 1667
Qy 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAaspAsnProHisLeuLeu 420
| | | | | : : : : :
Db 1668 ACTGGTGGCTTCCACCTGTCAACTTCAAGACTGCAAGGCCCAACAACCCGCGAGTCTCTG 1727
Qy 421 -----ThrIleGlnProAaspLeuSerThrThrThrThrThrThrThrThrThrThr 438
| | | | | : : : : :
Db 1728 CACCGCTCGCGCCCTCCAGACTCAACGGCCAGTCTGCGCATCTACCGCGGCGCTGTGTAT 1787
Qy 439 ProArgGlnAaspGlyProSerProLysPheGlnLeuThrAenGlyHisLeuLeuSerPro 458
| | | | | : : : : :
Db 1788 GCCCTGCGAGTCC-----GCCGACAGATCCCCATGACTAATTCGCCCTCTGCGATCCC 1844
Qy 459 LeuGlyGlyArgHisThrLeuHisSerSer----- 470
| | | | | : : : : :
Db 1845 CTGCCAGCCTCAAGATCAAGTCTATAACTCCAGCACCATCGTTCGGTCTGGGCTG 1904
Qy 471 -----ProThrSerGluAlaGluLupheVal 479
| | | | | : : : : :
Db 1905 GCTGATGAGCGGACCTGCTGGTGTCTCTCCCGCGGCGACGTACCCAGGCGGATTC--- 1961

Qy 480 SerArgLeuSerThrGlnAsnTyrPheArgSer----- 490
| | | | | : : : : :
Db 1962 TCCGGGACACCCATTTCCTGCACCTGGCAGTCCAGCCTTGGTTCACGACCTCCTG 2021
Qy 491 ---LeuProArgGlyThrSerAsnMetThrTyrGlyThrPheAenPheLeuGlyGlyArg 509
| | | | | : : : : :
Db 2022 GGCCTACTCGGACCCAGCAGCAGTGTACGCGGCACCTTGGTGGTGGAGGAAG 2081
Qy 510 LeuMetIleProAenThrGlyIleSerLeuLeuLeuProProAaspAlaIleProArgGly 529
| | | | | : : : : :
Db 2082 CTGAGCTTCCCGGCAAGGGGTGAGCTGTGTGTAACAAATGAGGACATTCGCCAGGC 2141
Qy 530 LysIleTyrGluIleTyrLeuThrLeuHisLysProGluAaspValArgLeuProLeuAla 549
| | | | | : : : : :
Db 2142 AAGTTCTATGACCTGTATCTACATATCAACAGGCCGGAAGCACC---CTCCACTTCA 2198
Qy 550 ---GlyCysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeu 568
| | | | | : : : : :
Db 2199 GAAGGTTCCAGACAGTATTGAGCCCTCGGTGACCTGTGGGCCACAGGCTACTCCTG 2258
Qy 569 ThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerProAaspSerTrpSer 588
| | | | | : : : : :
Db 2259 TGCAGCCTGTGTGCTCTACCGTCCCCACTGTCTGAAGTCATCGCTGGAGACTGGATC 2318
Qy 589 LeuArgLeuLysLysGlnSerCysGlySerTrpGluAaspValLeuHisLeuGlyGlu 608
| | | | | : : : : :
Db 2319 TTTGAGCTCAAGACCCAGGCCCATCAGGCCACTGGGAGGAGTGGTGACCTTGGATGAG 2378
Qy 609 GluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSerAlaCysTyrValPheThr 628
| | | | | : : : : :
Db 2379 GAGACCTCAACACACACCTGTCTACTGTCAGCTGGAGGCTAAGTCTCTGCCATCTCTG 2438
Qy 629 GluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAlaLysArg 648
| | | | | : : : : :
Db 2439 GACGAGCTGGTCTCTACGATTTCATGGGAGTCTTACTCTCGCTCTGCAAGTCAAGCGG 2498
Qy 649 LeuLysLeuLeuLeuPheAlaProValAlaCysThrSerLeuGluTyrAsnIleArgVal 668
| | | | | : : : : :
Db 2499 CTCAGCTGGCCATCTTGGCCCCAGCCCTCTGCACCTCCCTGGAGTATAGCCTCAGGTC 2558
Qy 669 TyrCysLeuHisAaspThrHisAaspAlaLeuLysGluValValGlnLeuGluLysGlnLeu 688
| | | | | : : : : :
Db 2559 TACTGTCTGGAGGACACACCTGTAGCAGTGAAGGAGTCTCTGGAGCTGGAGGACTCTG 2618
Qy 689 GlyGlyGlnLeuIleGlnGluProArgValLeuHisPheLysAaspSerTyrHisAsnLeu 708
| | | | | : : : : :
Db 2619 GGTGGCTACTTGGTGGAGGAGCCCAAGCCTTGTCTTTAAGGACAGTTACCAACCTA 2678
Qy 709 ArgLeuSerIleHisAaspValProSerSerLeuTrpLysSerLysLeuLeuValSerTyr 728
| | | | | : : : : :
Db 2679 CGCTCTCTCCATGACATCCCCCATCGCCACTGGAGGAGCAACTACTTGGCCAGTAC 2738
Qy 729 GlnGluIleProPheTyrHisIleTrpAsnGlyThrGlnArgTyrLeuHisCysThrPhe 748
| | | | | : : : : :
Db 2739 CAGGAGATTCCTTCTACCACTGTGATGGCAGCCAGCAGAGCCCTGCACCTGACCTTTC 2798
Qy 749 ThrLeuGluArgValSerProSerThrSerAaspLeuAlaCysLysLeuTrpValTrpGln 768
| | | | | : : : : :
Db 2799 ACCCTGAGAGGACATAGCTGGCCCTCCAGGAGTTCACCTGTAAAGTCTCGTGGCGGAC 2858
Qy 769 ValGluGlyAaspGlyGlnSerPheSerIleAsnPheAsnIleThrLysAaspThrArgPhe 788
| | | | | : : : : :
Db 2859 GTCGAGGGGAGGCCAGATTTTCAGCTGCACACACAGTGGCC---GAGACGCTGCT 2915
Qy 789 AlaGluLeuLeuAlaLeuGluSerGluAlaGly-----ValProAlaLeuValGlyPro 806
| | | | | : : : : :
Db 2916 GGCTCCCTGGATGCTCTCTGCTCTGCCCGGCAATGCCATCACACCCAGCTGGAGCCC 2975
Qy 807 SerAlaPheLysIleProPheLeuIleArgGlnLysIleSerSerLeuAaspPro 826
| | | | | : : : : :
Db 2976 TATGCTTCAAGATACCCCTGTCCATCCGCAAAAGATCTGCAGACGCTGGAGCGCCCC 3035
Qy 827 CysArgGlyAlaAaspTrpArgThrLeuAlaGlnLysLeuHisLeuAaspSerHisLeu 846

Db 3036 GATCCGGGGCAACGACTGGAGCTGTTGGCGCAGAACTGTCATGGACCGGTACCTA 3095
Qy 847 SerPhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTrpGluAlaArg 866
Db 3096 AACTACTTCCGCCAACCAAGCTAGTCCACAGGTGTCTATCTTAGACCTCTGGGAAGCTGG 3155
Qy 867 HisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnPro 886
Db 3156 CAACAGGATGACGGGACCTCAACAGCTTGGCCAGTGCCTTGGAGGAGATGGGCAAGAGT 3215
Qy 887 AspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 3216 GAGATGCTGTGTAGCCATGGCCACAGATGGCGGATTGC 3251

RESULT 13

US-10-087-684-1
; Sequence 1, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Sureeh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.

; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-1

Alignment Scores:

Pred. No.: 2,46e-260 Length: 2860

Score: 2563.50 Matches: 501
Percent Similarity: 69.08% Conservative: 147
Best Local Similarity: 53.41% Mismatches: 245
Query Match: 53.51% Indels: 45
DB: 17 Gaps: 15
US-10-624-932c-2 (1-898) x US-10-087-684-1 (1-2860)
Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuLeuAlaLafTrp--- 19
Db 59 ATGGGGGCCCGAGCGAGCTCGGGGCGCGTGTCTGTGGCACTGTCTCTCTGGAC 118
Qy 20 -----LeuArgGlySerGlyAlaGlnGln---SerAlaThrValAlaAsnProValPro 36
Db 119 CCGAGGCTGAGCCAAGCAGGCACTGATTCTGGCAGCGAGGTGCTCCTCTCTCCCG 178
Qy 37 GlyAlaAsnProAspLeuLeuProHisPheLeuValGluProGluAspValTyrIleVal 56
Db 179 TCAGCGCCAGCAGAGCGGCTGCGCTACTTCTTCGAGAGCCACAGACGCCTACTATTGTG 238
Qy 57 LysAsnLysProValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLys 76
Db 239 AAGAACAAAGCTGTGGAGCTCGCTCGCGCGCTTCCCGCCACACAGATCTACTTCAAG 298
Qy 77 CysAsnGlyGluTrpValArgGlnValAspHisValIleGluArgSerThrAspGlySer 96
Db 299 TGCACCGCGAGTGGGTGAGCCAGACGACCACTGTCACAGGAAAGCCCTGGATGAGGCC 358
Qy 97 SerGlyLeuProThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysVal 116
Db 359 ACCGGTCTGGGGTGGCGAGGTGCAGATCGAGTGTTCGGCGCAGCAGGTGGAGGACTC 418
Qy 117 PheGlyLeuGluGluTyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrLys 136
Db 419 TTTGGGCTGGAGGATTACTGTGCCAGTGTGGCTCGCGCTGGAGTCTCCGGGACCAACAA 478
Qy 137 SerGlnLysAlaTyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeu 156
Db 479 AGTCGCGGAGCTTACGTCCGATCGCTTACCTCGCAAGAACTTCGATCAGGAGCCTCTG 538
Qy 157 AlaLysGluValSerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIle 176
Db 539 GGCAAGAGGTGCCCTGGACCATGAGGTTCCTCTCAGTGCCTCGCGCGGAGGGGGTG 598
Qy 177 ProProAlaGluValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspPro 196
Db 599 CTTGTGGCGGAGTGGGAATGGCTCAAGAATGAGGATGTCTATCGACCCACCCAGGACAC 658
Qy 197 AsnValTyrIleThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThr 216
Db 659 AACTTCTGCTCACCATCGACCAACCTCATCTCCGCGAGCCCGCTGTCTGGACACT 718
Qy 217 AlaAsnTyrThrCysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAla 236
Db 719 GCCAATATACCTGCTGCGCAAGACATGTCGCCAAACGCCGCGAGCACCCTGCCACC 778
Qy 237 ValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAla 256
Db 779 GTCATGCTTACGTGAATGGCTGCTCCAGTGGCGAGAGTGGTGCACCCCTCTCCAAC 838
Qy 257 SerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsn 276
Db 839 CGCTGTGGCGAGGCTGGCAGAGCCGCCGAGCTTGCACCAACCCCGCTTCACTCAAC 898
Qy 277 GlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysPro 296
Db 899 GGAGGGGCGCTTCTGCGAGGCGCAGGCATTCACAAGACCGCCTGTCACCATCTGCCCA 958
Qy 297 ValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHis 316
Db 959 GTCGATGGGGCGTGGACGAGTGGCAAGTGGTTCAGCCTGAGCCTGTGATGTGGCCAC 1018
Qy 317 TrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGly 336

Db 1019 TGGCGTAGCCGAGTGTGATGCGCGCCCGCCAGACCGAGGCGGTGACTGACGCGG 1078
Qy ThrAspLeuAspThrArgAsnCysThrSerAspLeuCysValHis---SerAspSerGly 355
Db 1079 ACGTGTCTGACTCTAGACTGTGACAGATGGGCTGTGTCGCAACTGAGGAGGCTTCAGG 1138
Qy ProGluAspValAlaLeuTyrValGlyLeu---IleAlaValAlaValCysLeuValLeu 374
Db 1139 -----GATCGCGGCTGTATGCGGGCTGTGGTGGCCATCTTCGTGGTGTGCAATC 1192
Qy LeuLeuLeuValLeuLeuValTyrCysArgLysLysGluGlyLeuAspSerAspVal 394
Db 1193 CTCATGGCGGTGGGGTGTGTGTACCGCGCAACTGCGGTGATCTTCGACACAGACATC 1252
Qy AlaAspSerSer---IleLeuThrSerGlyPheGlnProValSerIleLysProSerLys 413
Db 1253 ACTGACTCATCTGCGCTGACTGGTGTGTTTCACCCCGTCAACTTTAAGACGGCAAG 1312
Qy AlaAspAsnProHisLeuLeu-----ThrIleGlnProAspLeuSerThrThrThr 431
Db 1313 CCCAGTAACCGCAGCTCTACACCCCTCTGTGCTCTCTGACCTGACAGCCGCGCGC 1372
Qy ThrTyrGlnGlySerLeuCysProArgGlnAspGlyProSerProLysPheGlnLeuThr 451
Db 1373 ATCTACCGCGGACCGGTGTATGCGCTGCGAGACTCC---ACCGACAAATCCCATGACC 1429
Qy AsnGlyHisLeuLeuSerProLeuGlyGlyArgHisThrLeuHisHisSerSerPro 471
Db 1430 AACTCTCTCTGCTGGACCCCTTACCGACCTTAAGGCTTAAGGCTTACAGCTCCGACACC 1489
Qy Thr-----SerGluAlaGluPheValSerArgLeuSerThrGln 485
Db 1490 ACGGGCTCTGGCGCCAGCTGCGAGATGGGCTGACCTGCTGGGGTCTTGGCCCTGGC 1549
Qy AsnTyr-----PheArgSer----- 490
Db 1550 ACATACCTTAGCGATTTCGCCGGGACACCCACTTCTGACCTGCGCAGCGCCAGCCTC 1609
Qy 491 -----LeuProArgGlyThrSerAsnMetThrTyrGlyThrPhe 503
Db 1610 GGTTCACGACGCTCTGGGCTGCTCCCGAGACCCAGGAGCAGCGTACGCGGACCTTT 1669
Qy AsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuLeuProPro 523
Db 1670 GGCTGCTGGTGGAGGCTCAGCATCCCGGACAGGGGTGCTGCTGGTGGCCCAT 1729
Qy AspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLysProGluAsp 543
Db 1730 GGAGCCATTCCCGAGGCAAGTTCTACGAGATGTATCTACTCATCAACAGGCGAGAAAT 1789
Qy ValArgLeuProLeuAla---GlyCysGlnThrLeuLeuSerProIleValSerCysGly 562
Db 1790 ACC---CTGCGCTTTTCAGAGGAGACCCAGACAGTATTAGCCCTCGGTGACTGTGGA 1846
Qy ProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluPro 582
Db 1847 CCCACAGGCTCTCTGCTGTGCGGCTCATCTCACCATGCCCATCTGTGCGGAGTC 1906
Qy SerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySerTrpGluAsp 602
Db 1907 AGTCCCGTGACTGGATCTTTGAGCTCAAGACCCAGGCCACCCAGGGCCACTGGGAGAG 1966
Qy ValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSer 622
Db 1967 GTGTGACCTGGATGGAGACCCCTGAACACACCCCTGCTACTGCCAGCTGGAGCCAGG 2026
Qy AlaCysTyrValPheThrGlnGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSer 642
Db 2027 GCTGTACATCTCTGTCGACGAGCTGCGGACCTACGTGTTCAGCGGCGAGTCTATTCC 2086
Qy ValAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThrSerLeu 662

Db 2087 CGCTCAGCAGTCAAGCGGCTCCAGCTGCGCGCTCTTTCGCCCGCCCTCTGACACCTCCCTG 2146
Qy GluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValVal 682
Db 2147 GAGTACAGCTCCGGGTCTACTGCTGGAGGACACGCTGTAGCACTGAAGAGGAGTGTCTG 2206
Qy GlnLeuGluLysGlnLeuGlyGlyGlnLeuGlnGluProArgValLeuHisPheLys 702
Db 2207 GAGCTGGAGCGGACTCTGGCGGATACTTGGTGAGGAGCGCAACCGCTAATGTTCAAG 2266
Qy AspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrpLysSer 722
Db 2267 GACAGTTACCAACACCTGCGCTCTCCCTCCATGACCTCCCATGCGCATTCGAGGAGC 2326
Qy LysLeuLeuValSerTyrGlnGluLeuProPheTyrHisIleTyrAsnGlyThrGlnArg 742
Db 2327 AGCTGTGCGCAAAATACAGGAGATCCCTTCTATCACATTTGGAGTGGGAGCGCAGAG 2386
Qy TyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeuAlaCys 762
Db 2387 GCCTTCACCTGCATTTTCACTGGAGGAGGACAGCTTGGCTCCACAGAGTCACCTGC 2446
Qy LysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIle 782
Db 2447 AAGATCTGCGTGGCGCAAGTGAAGGGGAGGCGGCAGATATTCAGCTGCATACCACCTG 2506
Qy ThrLysAspThrArgPheAlaGluLeuAlaLeuGluSerGluAlaGly-----Val 800
Db 2507 GCA---GAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2563
Qy ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
Db 2564 ACCACCGAGCTGGGACCTTATGCTTCAAGATCCCATCTCCATCCCGCAGAGATATGC 2623
Qy SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
Db 2624 AACAGCTAGATGCCCACTCACGGGCAATGACTGGGGAGTGTAGCACAGAGCTC 2683
Qy HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2684 TCTATGACCGGTACCTGAAATTTTCCACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 2743
Qy AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2744 GACCTCTGGAGAGCTTGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2803
Qy AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2804 GAGGAGATGGGCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2857

RESULT 14
US-10-087-684-3
; Sequence 3, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Miller, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Sheno, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 8, 2005, 02:39:30 ; Search time 10019 Seconds

(without alignments)
3411.689 Million cell updates/sec

Title: US-10-624-932c-2

Perfect score: 4791

Sequence: 1 MAYRPGMLPALLGIVLAWL.....AVAGLGOPDAGLFTVSEAC 898

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q=/cgn2_1/USPTO_spoil_p/US10624932/runat_03082005_110053_3214/app_query.fasta_1.1095
-DB=EST -QPM=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932@cgn 1 1 5180 @runat_03082005_110053_3214 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2767.5	57.8	3790	3 AK031655	AK031655 Mus muscu
2	2747	57.3	2802	9 AY406491	AY406491 Homo sapi
3	2733	57.0	2791	9 AY406493	AY406493 Mus muscu
4	2572.5	53.7	3866	3 AK018177	AK018177 Mus muscu
5	2422.5	48.9	2532	9 AY411749	AY411749 Mus muscu
6	2326.5	48.6	2532	9 AY411747	AY411747 Homo sapi
7	2244	46.8	2802	9 AY406492	AY406492 Pan trogl
8	2111	44.1	2775	9 AY401471	AY401471 Mus muscu
9	2104	43.9	2775	9 AY401469	AY401469 Homo sapi

10	1917.5	40.0	2532	9	AY411748	AY411748 Pan trogl
11	1884.5	39.3	1532	3	BC033727	BC033727 Homo sapi
12	1591.5	33.2	2507	9	AY401470	AY401470 Pan trogl
13	1524	31.8	1852	3	CR598115	CR598115 full-length
14	1402	29.3	1034	4	BI758231	BI758231 603029876
15	1349	28.2	818	4	BI818609	BI818609 60303362
16	1274.5	26.6	874	5	BQ689148	BQ689148 AGENCOURT
17	1270	26.5	788	1	AI951556	AI951556 wv36f04.X
18	1269	26.5	788	6	CA317532	CA317532 UI-M-FW0-
19	1268.5	26.5	889	5	BQ691915	BQ691915 AGENCOURT
20	1252	26.1	756	5	BU612387	BU612387 UI-M-EW0-
21	1252	26.1	796	5	EX348193	EX348193 BX348193
22	1206	25.2	1175	2	BF530640	BF530640 602071931
23	1200	25.0	751	7	CF735550	CF735550 UI-M-HB0-
24	1197	25.0	749	7	CF735417	CF735417 UI-M-HB0-
25	1187	24.8	723	5	BU613458	BU613458 UI-M-EW0-
26	1187	24.8	856	7	CN164143	CN164143 994266 MA
27	1148	24.0	678	6	CA749784	CA749784 UI-M-FD0-
28	1142.5	23.8	934	2	BF311804	BF311804 601897316
29	1133	23.6	853	5	BX364574	BX364574 BX364574
30	1119.5	23.4	859	2	BF311896	BF311896 601897733
31	1093	22.8	675	6	CA315487	CA315487 UI-M-FW0-
32	1033	21.6	977	5	BX345407	BX345407 BX345407
33	1032	21.5	604	2	BE314370	BE314370 601147261
34	1024	21.4	601	1	AL516580	AL516580 AL516580
35	1022.5	21.3	843	4	BG913440	BG913440 602811321
36	997.5	20.8	900	5	BX345406	BX345406 BX345406
37	992.5	20.7	1072	5	BX422753	BX422753 BX422753
38	984	20.5	720	1	AI959236	AI959236 fd25910.Y
39	979	20.4	572	7	CR554569	CR554569 DKF2p4591
40	978	20.4	679	7	CO045001	CO045001 UI-M-G10-
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43	900	18.8	824	4	BI737024	BI737024 603360874
44	895	18.7	848	4	BI700830	BI700830 ib81904.Y
45	879.5	18.4	608	4	BM487397	BM487397 pgm2n.pk0

ALIGNMENTS

RESULT 1

AK031655

LOCUS

DEFINITION

AK031655 3790 bp mRNA linear HTC 03-APR-2004
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030473H24 product:unc5 homolog (C.
elegans) 3, full insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

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AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

AK031655 3790 bp mRNA linear HTC 03-APR-2004
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030473H24 product:unc5 homolog (C.
elegans) 3, full insert sequence.
AK031655 GI:26327502
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Ozaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 MEDLINE
 PUBLISHED
 11076861

REFERENCE

AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

TITLE

REFERENCE

AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

TITLE

REFERENCE

AUTHORS

Nature 420, 563-573 (2002)
 6 (bases 1 to 3790)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kaga, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

FEATURES

source

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CDS

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 GQQLLEPRLALFKGSIHNLRLSIHDIAHSLKSLAKYQEI PFPHIWSGSGRNLC
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ORIGIN

Alignment Scores:	8,47e-236	Length:	3790
Pred. No.:	2767.50	Matches:	522
Score:	72.58%	Conservative:	153
Percent Similarity:	56.13%	Mismatches:	208
Best Local Similarity:	57.76%	Indels:	47
Query Match:	3	Gaps:	10
DB:			

US-10-624-932c-2 (1-898) x AK031655 (1-3790)

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QY	29	Ala-----ThrValAlaAenProValProGlyAlaAenProAsnProAsnLeuProHis	45
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QY	46	PheLeuValGluProGluAspValTyrIleValIleAsnIleValLeuValCys	65
DB	307	TTCTCATTTAGCGCCGAGGAGCTTACATTGTGAAGAACAGCTGTGAACCTGTATTGT	366
QY	66	LysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyLeuTrpValArgGlnVal	85
DB	367	AAAGCCAGCCCTGCCACCCAGATCTACTTCAAGTGCACAGCAGTGGTTCATCAGAAG	426
QY	86	AspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGluValArg	105
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QY	106	IleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGluTyrTrpCysGln	125
DB	487	ATTGAGATTTCAGCCAGCAGGTTGGAGGAACTGTTGGGCTGAAGATTACTGTCGACAG	546
QY	126	CysValAlaTrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArgIleAla	145
DB	547	TGTTGGCTTGGAGCTCAGCAGGCACTACGAGAGTTCGGAAGGCATACGTCGCATTGCG	606
QY	146	ArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGluGlnGly	165
DB	607	TATCTCGGAAGACATTCGAGCAGGAAACCTTTGGGAAGAGAGTCTCTTGGAGCAGGAA	666
QY	166	IleValLeuProCysArgProGluGlyIleProProAlaGluValGluTrpLeuArg	185
DB	667	GTCTTACTCAAGTCTGGCCACCTGAAGGATCCCAAGTGTGAGTAGAATGGCTAAG	726
QY	186	AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer	205
DB	727	AATGAAGACATAATTCATCTGCTGAAGATCGGAACCTTTTATATTACTATCGATCAAC	786
QY	206	LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAlaLysAsn	225
DB	787	CTGATCATCAAGCAAGCCGACTCTCAGATACAGCAAAATATATACCTGTGTGTCACAAAAT	846
QY	226	IleValAlaArgArgArgSerAlaSerAlaAlaValIleValTyrValLeuGlyTrp	245
DB	847	ATTGTTGCCAAGAAAAAGAACACCAAGCCACTGTCTGTGTATGTATATGTGGCTGG	906
QY	246	SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg	265
DB	907	TCCACCTGGACAGAGTGGTCTGTGTGTAAACAGCCGCTGTGGGCGAGGATATCAGAAACGC	966

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Db	967	ACA	AGA	ACC	CTC	ACC	CAAC	CCC	AGC	CCC	CACT	CAAT	TGG	TGG	GCT	TTCT	GTG	AGG	GGC	GAG	1026
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Db	1087	AAA	TGG	TCA	ACT	TGG	GACT	GAAT	GCA	CCC	CACT	GGCG	CAG	AGG	GGG	AGT	GT	PAC	AGC	ACA	1146
Qy	326	Ala	Pro	Arg	Asn	Gly	Gly	Leu	Glu	Cys	Gln	Gly	Thr	Asp	Leu	Asp	Thr	Arg	Asn	Cys	345
Db	1147	GCC	CCC	AAGA	AC	GGG	GST	TAAG	ACT	GTG	ATG	CGC	TGG	TCT	CCA	AT	CC	AGA	ACT	GC	1206
Qy	346	Ser	Asp	Leu	Cys	Val	His	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	351
Db	1207	GAT	GGG	CTGT	GAT	GAC	GGG	ATT	CAT	TTAC	CCC	ATT	CACT	GAG	CAC	AG	CCCC	AG	AA	T	1266
Qy	352	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	365
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Qy	366	Ile	Ala	Val	Ala	Val	Cys	Leu	Val	Leu	Leu	Leu	Val	Leu	Ile	Leu	Val	Tyr	Cys	Arg	385
Db	1327	ATC	GCT	GT	AAC	AGT	CTG	TCT	GGC	GAT	CAC	TGTT	GTG	TGG	CCCT	TGTT	GTG	TAT	CG	AA	1386
Qy	386	Lys	Leu	Glu	Gly	Leu	Asp	Ser	Asp	Val	Ala	Asp	Ser	Ser	Ile	Leu	Thr	Ser	Gly	Phe	405
Db	1387	AAC	CAC	CGT	GACT	TTG	AGT	CTG	CA	TAT	CA	TG	ACT	CTC	CAG	CAC	TCA	AT	GCG	GGT	1446
Qy	406	Pro	Val	Ser	Ile	Leu	Pro	Ser	Lys	Ala	Asp	Asn	Pro	His	Leu	Leu	Thr	Ile	Gln	Pro	425
Db	1447	CCT	GTG	AAC	ATCA	AGG	CTGCC	ACA	AGAT	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	1497
Qy	426	Leu	Ser	Thr	Thr	Thr	Thr	Tyr	Gln	Gly	Ser	Leu	Cys	Pro	Arg	Gln	Asp	Gly	Pro	Ser	445
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Qy	446	Pro	Lys	Phe	Gln	Leu	Thr	Asn	Gly	His	Leu	Ser	Pro	Leu	Gly	Gly	Arg	His	Thr	465	
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Qy	466	Leu	His	Ser	Ser	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	481	
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Qy	482	Leu	Ser	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	Arg	489
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Qy	490	Ser	Leu	Pro	Arg	Gly	Thr	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	507
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Qy	508	Gly	Arg	Leu	Met	Ile	Pro	Asn	Thr	Gly	Ile	Ser	Leu	Leu	Ile	Pro	Pro	Asp	Ala	Leu	527
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Qy	528	Arg	Gly	Leu	Ser	Ile	Tyr	Glu	Ile	Tyr	Leu	Thr	Leu	His	Leu	Ser	Pro	Glu	Val	Leu	547
Db	1855	CAG	GGG	AG	AGT	CTAT	GA	AA	TAT	GTAT	G	ACT	GTAC	AG	AA	AA	AA	AA	AA	AT	1914
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Qy	568	Leu	Thr	Arg	Pro	Val	Ile	Leu	Ala	Met	Asp	His	Cys	Gly	Glu	Pro	Ser	Pro	Asp	Ser	587
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Qy	588	SerLeuArgLeuLysLysGlnSerCysGluGlySerTrpGluAspValLeuHisLeuGly	607
Db	2035	AAAGTCCAGCTCAAAAAGAGGAGCAATGGGAGGATGTGTGGTGGTGGG	2094
Qy	608	GluGluAlaProSerHisLeuTyTrpCysGlnLeuGluAlaSerAlaCysTyValPhe	627
Db	2095	GAGGAGAACTTCACACCCCTGTTACATTACGTGATGCAGAGCTTGCCATATCTCTC	2154
Qy	628	ThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAlaLys	647
Db	2155	ACAGAGAACTCAGTACCTATGCTGTTGGGAGTCCACCAAGCAGCTGCCAAG	2214
Qy	648	ArgLeuLysLeuLeuLeuPheAlaProValAlaCysThrSerLeuGluTyAsnIleArg	667
Db	2215	CGTCTTAAACTGGCCATCTTTGGGCCCTCTGCTGCTCTTCCCTGGAGTACAGCATTAGA	2274
Qy	668	ValTyCysLeuHisAspThrHisAspAlaLeuLysGluValValGlnLeuGluLysGln	687
Db	2275	GTCCTACTGCTTGGATGACACACAGGATGCCCTGAAGGAGTCTTACAACTTGGAGAGGCAA	2334
Qy	688	LeuGlyGlnLeuIleGlnGluProArgValLeuHisPheLysAspSerTyHisAsn	707
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Qy	708	LeuArgLeuSerIleHisAspValProSerSerLeuTrpLysSerLysLeuLeuValSer	727
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Qy	728	TyrGlnGluIleProPheTyHisIleTrpAsnGlyThrGlnArgTyLeuHisCysThr	747
Db	2455	TATCAGAAATTCATTTTACCACATCTGAGTGGCTCTCAAGAAACCTTCCACTGCACC	2514
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Qy	788	PheAlaGluLeuAlaLeuGluSerGluAlaGlyValProAlaLeuValGlyProSer	807
Db	2635	GGCATCCAGTACTCTCTCTGGACCTGTGTAGTACCATCACCACTGTCCCGGACCAAGT	2694
Qy	808	AlaPheLysIleProPheLeuIleArgGlnLysIleSerSerLeuAspProProCys	827
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Qy	828	ArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSer	847
Db	2755	ACAAGAGGCCATGACTGGAGGATGCTGGCCATAAACTCAACCTGGACAGGTACTTGAAT	2814
Qy	848	PhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTrpGluAlaArgHis	867
Db	2815	TACTTTCCCAACCAATCGACCCCACTGGCGTAACTCTGGATCTTTGGGAAGCAGCAAC	2874
Qy	868	PheProAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAsp	887
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Qy	888	AlaGlyLeuPheThrValSerGluAlaGlu	897
Db	2935	ACAGTGGTGTTACTTGGCAGCAGAGGACAG	2964
RESULT 2			
LOCUS	AY406491		
DEFINITION	Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,	2802 bp	DNA linear
ACCSSION	AY406491		
VERSION	AY406491.1		
KEYWORDS	GI:39762465		
SOURCE	Homo sapiens (human)		

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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2802)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2802)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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/mol_type="genomic DNA"
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ORIGIN
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Score: 2747.00 Matches: 514
Percent Similarity: 73.17% Conservative: 154
Best Local Similarity: 56.30% Mismatches: 215
Query Match: 57.34% Indels: 30
DB: 9 Gaps: 10

US-10-624-932C-2 (1-898) x AY406491 (1-2802)
QY 9 ProAlaLeuGlyIleValLeuAlaAtrLeuArgGlySerGlyAlaGlnSer 28
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
76 CTTGCCCTG-----GCCCTGCTCAGCCGCGGCACTGGCTCCGCCGCCAAGATGAT 129
QY 29 -----AlaThrValAlaAsnProValProGlyAlaAsnProAspLeuProHis 45
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
130 GACTTTTTTCATGAATCCCGAGAACTTTTCTCTGATCCACCTGAGCCTCTGCCACAT 189
QY 46 PheLeuValGluProGluAspValTyrIleValIysAsnLysProValLeuValCys 65
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
190 TTCCTATTGAGCCTGAAGAAGCTTATATTGTGAAGAAATAAGCTGTGAACCTGTACTGT 249
QY 66 LysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpValArgGlnVal 85
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
250 AAGCAGAGCCCTGCCACCCAGATCTATTTCAGTGTAAATAGTGAATGGGTTCATCAGAAG 309
QY 86 AspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGluValArg 105
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
310 GACCACATAGTAGAAGAGTAGATGAACCTTCCGGTCTCATTTGTCGGGAAGTGAGC 369
QY 106 IleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGluTyrTrpCysGln 125
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370 ATTGAGATTTCCGGCCAGCAAGTGAAGAACTCTTTGGACCTGAAGATTACTGGTGCAG 429
QY 126 CysValAlaTrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArgIleAla 145
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QY 146 -----ArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
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Qy 525 AlaIleProArgGlyLysIleGlyLeuThrLeuHisLysProGluAspVal 544
Db 1678 GCCATTCCCAAGGAGAGTCTAGAAATGATGTGACTGTACACAGGAAGAACAATATG 1737
Qy 545 ArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyProPro 564
Db 1738 AGGCACCCATGGATGACTCTCAGACACTTTTGACCCCTGTGGTGTGAGCTGTGGCCCCCA 1797
Qy 565 GlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerPro 584
Db 1798 GGAGCTCTGTCTCACCCGCGCAGTGTCTCTACTATGCATCATCTGCGCAGACCCCAATACC 1857
Qy 585 AspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySerTrpGluAspValLeu 604
Db 1858 GAGGACTGGAAATACTCTCAGAACCCAGCAGCAGGACAGTGGGAGATGTGGTG 1917
Qy 605 HisLeuGlyGluGluAlaProSerHisLeuTyrrCysGlnLeuGluAlaSerAlaCys 624
Db 1918 GTGTGCGGAGGAGAACTTCACACCCCTGTCTACTATTCAGCTGGATGCAGGCTGTC 1977
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Qy 665 AsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValIleGlnLeu 684
Db 2098 AGCATCGAGTCTACTGTCTGTGATGACACCCAGATGCCCTGAAGAAATTTTACATCTT 2157
Qy 685 GluLysGlnLeuGlyGlnLeuIleGlnLpArgValLeuHisPheLysAspSer 704
Db 2158 GAGACAGATGGGAGGACAGCTCTAGAGAACTTAAGGCTCTTCATTTTAAAGGCAGC 2217
Qy 705 TyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrpLysSerLysLeu 724
Db 2218 ACCCACAACTTGCCTCTGTAATTCAGATATCCCATTCCTCTGGAAGAGCAAAATG 2277
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Db 2278 CTGCTAAATATCAGGAATTCATTTTACATGTTTGGAGTGTATCTCAAGAAACCTG 2337
Qy 745 HisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLeu 764
Db 2338 CACTGCACCTTCACTCTGGAAGATTTAGCTGGAACACAGTGGAGCTGGTTTGCANAATC 2397
Qy 765 TrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLys 784
Db 2398 TGTGTGGCGGAGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2457
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Db 2578 GCGCCCGCAGACGAGGCGCATGACTGGAGGATGCTGGCCCATATAGCTCAACCTGCAGCAG 2637
Qy 845 HisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTrpGlu 864
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LOCUS AY406493
DEFINITION Mus musculus UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION AY406493
VERSION AY406493.1 GI:39762467
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2791)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2791)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
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gene
ORIGIN

Alignment Scores:
Pred. No.: 6,3e-233 Length: 2791
Score: 2733.00 Matches: 518
Percent Similarity: 73.41% Conservative: 153
Best Local Similarity: 56.67% Mismatches: 208
Query Match: 57.04% Indels: 35
DB: 9 Gaps: 11

US-10-624-932C-2 (1-898) x AY406493 (1-2791)
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Db 76 CCTGCCCTG-----GCCCTGTCTAAGCGCCAGTGGCACCCTCCCGCTCAAGATGAT 129
Qy 29 Ala-----ThrValAlaAsnProValProGlyAlaAsnProAspLeuLeuProHis 45
Db 130 GAATTTTTCAGAACTCCCGAAGAACTTTTCCATCTGACCCACTGTGACCATTCGCCACAC 189
Qy 46 PheLeuValGluProGluAspValTyrIleValLysAsnLysProValLeuValCys 65
Db 190 TTCTCTATTGAGCCCGAGGAGCTTACATTGTGAGAACAGGCTGTGAACCTGTATTGT 249
Qy 66 LysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpValArgGlnVal 85
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QY     106  IleAsnValSerArgGlnGlnValGluValPheGlyLeuGluGluTyrTrpCysGln 125
Db      370 ATTGAGATTTCAGCCGACGAGGTGGAGAACTGTTGGGCTGAGAGTACTGTTGCCAG 429
QY     126  CysValalaTrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArgIleAla 145
Db      430 TGTGTGGCTCGAGCTCAGCAGCAGCTACGAGAGTGGAGGATACGTCGCGCATTTGG 489
QY     146  -----ArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
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QY     164  GlnGlyIleValLeuProCysArgProProGlu-GlyIleProAlaGluValGluTr 183
Db      550 CAGGAGTCTTATCCAGTGTGGCCACCTGAAGGGA-----TCCGTAGAATG 597
QY     183  pLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgG 203
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QY     243  YGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpG 263
Db      778 TGGCTGTCTCACCTGGACAGAGTGTCTGTGTGTAAACAGCCGCTGTGGCGAGGATATCA 837
QY     263  nLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluG 283
Db      838 GAAACGCACAGAAACCTGCAACCAACCCAGCCCACTCAATGGTGGGCGCTTCTGTGAGGG 897
QY     283  YGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPr 303
Db      898 GCAGAGTGTCCAGAAATACATGCATCTACTATTATGTCAGTGCATGTAGTGGACTTC 957
QY     303  oTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCys 323
Db      958 ATGGAGCAAAATGTTCAACCTGTGGGACTGGAATGCACCCACTGGCGCAGGAGGTGTAC 1017
QY     323  rAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThrArgAs 343
Db      1018 AGCACCAGCCCCCAAGAACGGGGGTAGGACTGTGTATGGCTCTCTCCATCCAAATCCAAGAA 1077
QY     343  nCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyrVa 363
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QY     363  lGlyLeu---IleAlaValAlaValCysLeuValLeuLeuLeuValLeuIleLeuVa 382
Db      1138 GGGGATTGTGATCGCTGTAACAGTGTCTGTGGGATCAGTGTGTGGTGGCCCTGTTGT 1197
QY     382  lTyrCysArgLysGlyGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSe 402
Db      1198 GTATCGGAAGAACCCCGTGACTTTTGAGTCTGATCATCTATTCATCTCTCAGCACTCAATGG 1257
QY     402  rGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeuThrI 422
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QY     422  eGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThrThr 442
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QY     462  yArgHisThrLeuHisHisSerSer-----ProThrSerSerGluAlaGluGluPh 478
Db      1426 GAAAATCAAGTGTACACAGCTCAGGTGCTGTCTCTCTCAGGATGACCTTCCCGAGTT 1485
QY     478  eValSerArgLeuSer-----ThrGlnAsnTyrPhe----- 488
Db      1486 CTCATCCAAATGTTCACCCAGATGACCCAGTCCCTTGTGTAGAGATGAGGCCCTTAACT 1545
QY     489  -----ArgSerLeuProArgGlyThr-----SerAsnMetThrTyrGlyThrPheAs 504
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QY     524  pAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLysPProGluAspVa 544
Db      1666 GGCATTCCTCTCAGGGGAGAGTCTATGAAATGTATGTGACTGTACACAGGAAAGAAATAT 1725
QY     544  lArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyProPr 564
Db      1726 GAGGCCCCATGGAAGACTCTCAGACCCCTACTTACCCCTGTGTGTGAGCTGTGGGCTCC 1785
QY     564  oGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerPr 584
Db      1786 TGGAGCTGTCTGACCCGCGCTGTCTCTCTCTCTGATCACTGTGCAGACCCAGCAC 1845
QY     584  oAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrpGluAspValle 604
Db      1846 CGAGGACTGGAAGATCCAGCTCAAAAACCCAGGCAGTGCAGGACAAATGGAGAGTGTGT 1905
QY     604  uHisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSerLaCy 624
Db      1906 GGTGGTGTGGGAGGAGAACTTCACACCCCTGTGTATTCAGTGCATGCAGAGGCTTG 1965
QY     624  sTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerVala 644
Db      1966 CCATATCTCCACAGAGAACCTCAGTACCTATGCCCTGTGGTGGGCGAGTCCACCAAGC 2025
QY     644  aAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThrSerLeuGluTyr 664
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QY     664  rAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValGlnLe 684
Db      2086 CAGCATTAGAGTCTACTGCTGGATGACACACAGGATGCCCTGAAGAAAGTTCACAACT 2145
QY     684  uGluLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHisPheLysAspSe 704
Db      2146 GGNAGAGCAATGGGAGGACAGCTCTCAGAGAACCCCAAGGCTCTTCATTTTAAAGCAG 2205
QY     704  rTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrpLysSerLysLe 724
Db      2206 CATCCACAACCTGGCGCTGTCTATTATGACATCGCCCATTCCTCTGGAAGACAAAT 2265
QY     724  uLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThrGlnArgTyrLe 744
Db      2266 GCTGGCTAAGTATCAGAAATTCATTTTACCACATCTGAGTGGCTCTCAAGAAACCT 2325
QY     744  uHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLe 764
Db      2326 CCACTGCACCTTCACTCTGGAAGACTCAGCCTAAACACACAGTGGAACTGTTTGCAACT 2385
QY     764  uTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLy 784
Db      2386 CTGTGTGCGCGAGTGTGAAGGAGAGGGCAGATCTTCCAGCTCAACTGTACTGTCTCAGA 2445
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ORIGIN

Alignment Scores:

Pred. No.: 2,52e-218 Length: 3866
 Score: 2572.50 Matches: 505
 Percent Similarity: 68.80% Conservative: 150
 Best Local Similarity: 53.05% Mismatches: 236
 Query Match: 53.69% Indels: 61
 DB: 3 Gaps: 15

US-10-624-932C-2 (1-898) x AK018177 (1-3866)

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 Qy 20 -----LeuArgGly-----SerGlyAlaGlnGlnSerAlaThrValAlaAasn 33
 Db |||||
 Qy 477 CCGACACCGAGCCTAGCAGCGTGTACTCTGTCTGGCCAG-----GTGCTCCCGAGC 527
 Db |||||
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 Db |||||
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 Db |||||
 Qy 54 TyrIleValLysAasnLysProValLeuValCysLysAlaValProAlaThrGlnIle 73
 Db |||||
 Qy 588 TACATCGTAAAGAACAGCCAGTGGAACTGCACTGCAGAGCCTTCCCTGCCACGAGATC 647
 Db |||||
 Qy 74 PhePheLysCysAasnGlyGluTrpValArgGlnValAaspHisValIleGluAArgSerThr 93
 Db |||||
 Qy 648 TACTTCAAGTGAATGCGAGTGGTGCAGCAGAAATGACCACGTACACAGAGAGAGCCTG 707
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 Qy 94 AspGlySerSerGlyLeuProThrMetGluValArgIleAasnValSerArgGlnGlnVal 113
 Db |||||
 Qy 708 GATGAGCCACAGCCTTGGCGGTGCGAGAGTGGATGAGGTGTCAGCGAGCAAGTG 767
 Db |||||
 Qy 114 GluLysValPheGlyLeuGluGluTyrTrpCysGlnCysValAlaTrpSerSerSerGly 133
 Db |||||
 Qy 768 GAGGAACCTCTCGGCTCGAGGACTACTGTGTCAGTGGCTGGCTGGAGCTCTTCGGGA 827
 Db |||||
 Qy 134 ThrThrLysSerGlnLysAlaTyrIleArgIleAlaArgLeuArgLysAasnPheGluGln 153
 Db |||||
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 Db |||||
 Qy 154 GluProLeuAlaLysGluValSerLeuGluGlnGlyIleValLeuProCysArgProPro 173
 Db |||||
 Qy 888 GAGCCTCTGCCAGGAGGTTACCTTGGATCATGAGGTCTCTTCGAGTCCGCCACCC 947
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 Qy 174 GluGlyIleProProAlaGluValGluTrpLeuArgAasnGluAaspLeuAaspProSer 193
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 Qy 948 GAGGAGTGCTGTGGCTGAGTGGATGCTCAAGAAATGAAGATGTCATTGACCCCGCT 1007
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 Qy 194 LeuAaspProbenValTyrIleThrArgGluHisSerLeuValValArgGlnAlaArgLeu 213
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 Qy 1008 CAGGACACTAATCTCTCTGCTCACCATTGACCACCAACCTCATCTCCGCCAGCGCGCTC 1067
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 Qy 214 AlaaspThrAlaAasnTyrThrCysValAlaLysAasnIleValAlaArgArgSerAla 233
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ACCESSION AY411749
VERSION AY411749.1 GI:39767717
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE 1 (bases 1 to 2532)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2532)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity: 53.60% Mismatches: 205
Query Match: 48.89% Indels: 51
DB: 9 Gaps: 12
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QY 119 LeuGluGluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGln 138
Db 61 CTCGAGGACTACTGTGTCAGTGTGCTGCTGAGCTCTTGGGGAACATCAAGAGTCGC 120
QY 139 LysAlaTyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLys 158
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QY 159 GluValSerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProPro 178
Db 181 GAGGTACCTTGGATCATGAGGTCTTCTGCACTGCGCCACCGGAGGAGTGCCTGTG 240
QY 179 AlaGluValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnVal 198
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AUTHORS       1 (bases 1 to 2532)
              Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE         Inferring nonneutral evolution from human-chimp-mouse orthologous
              gene trios
JOURNAL       Science 302 (5652), 1960-1963 (2003)
PUBMED       14671302
AUTHORS       2 (bases 1 to 2532)
              Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE         Direct Submission
JOURNAL       Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
COMMENT       This sequence was made by sequencing genomic exons and ordering
              them based on alignment.
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Qy 505 PheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProProAsp 524
Db 1618 TNGCTGGNNNNACCTTATTTGTTCCAAATTCAGGAGTCAGCTTGCTGTATCCCGCTGG 1677
Qy 525 AlaIleProArgGlyLysIleTyrGluIleTyrGluIleThrLeuHisLysProGluAspVal 544
Db 1678 GCCATTCCCAGGGAGAGTCTACGAATGTATGTACTGTACACAGGAAGAACAATATG 1737
Qy 545 ArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyProPro 564
Db 1738 AGGCCACCCATGGATGACTCTCAGACACTTTTGACCCCTGTGGTGAGCTGTGGGCCCA 1797
Qy 565 GlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerPro 584
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Qy 585 AspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySerTrpGluAspValLeu 604
Db 1858 GAGGACTGGAAATATCTGCTCAGAACACGACGACACGAGGACAGTGGAGATGTGTG 1917
Qy 605 HisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSerAlaCys 624
Db 1918 GTGTGCGGGGAGAAACTTCACCACCCCTGTCTACATTTCAGCTGGATGCGAGGCGCTGC 1977
Qy 625 TyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAla 644
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Qy 665 AsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValValGlnLeu 684
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Qy 685 GluLysGlnLeuGlyGlnLeuLeuLeuGlnGlnProArgValLeuHisPheLysAspSer 704
Db 2158 GAGACAGATGGAGGACAGCTCTCTGAAAGACTTAGAAGACCTAAGGCTCTTCAATTTAAAGGCG 2217
Qy 705 TyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrpLysSerLysLeu 724
Db 2218 ACCACAACTGGCGCTGTCAATTCAGATATGCCCATTCCTCTCTGGAAGGCAATTTG 2277
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RESULT 8
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DEFINITION Mus musculus HCM0901 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY401471
VERSION   AY401471.1
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2775)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
          Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
          Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene trices
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302
REFERENCE 2 (bases 1 to 2775)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
          Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
          Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Direct Submission
          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
          This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
FEATURES  Location/Qualifiers
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Alignment Scores:
Pred. No.:      3,07e-177      Length:      2775
Score:          2111.00      Matches:     413
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Best Local Similarity: 45.29%      Mismatches: 293
Query Match:    44.06%      Indels:      56
DB:              9      Gaps:          12

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Qy      44 ProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysProValLeuLeu 63
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Db      106 CCTCATTTTCATCGAGGAGCCGAGAGTGCATCATCAAGAGCAACCCGATTGCACATC 165
Qy      64 ValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpValArg 83
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Qy      104 ValArgIleAsnValSerArgGlnValGluLysValPheGlyLeuGluGluTyrTrp 123
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Db      286 GTGTTTATCAATGTCACAGGAGCAAGTGGAGGACTTCCATGGCCAGAGGACTACTGG 345
Qy      124 CysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAlaTyrIleArg 143
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Db      346 TGCACGTGTGTAGCTGGAGCCACCTCGGGAACGTCCAAGAGTAGGAGGCAATCTGTGCGC 405
Qy      144 IleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
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Db      406 ATAGCCCTATTACGGAAAACCTTTGAACAGATCCACAGGAGGAGGTTCTCTATTGAA 465
Qy      164 GlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrp 183
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Qy      204 HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 223
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Qy      224 LysAsnIleValAlaAlaArgArgSerAlaSerAlaAlaValIleValTyrValAsnGly 243
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Db      646 GCCAACAATCGTGGCCAAGAGGAGGAGCCCTCTCAGCAACTGTGGTGTCTACGTGAATGGA 705
Qy      244 GlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGln 263
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Db      706 GGCCTGTCTCTCTCTGGCAGAGTGGTCTGCAATGTTCGCTGTGTGTAGAGATGGCAG 765
Qy      264 LysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGly 283
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      766 AAACGTTCCGGACCTGCACCAACCCCGCTCTCTCAATGGTGGGCGCTTTTGTGAGGGA 825
Qy      284 GlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPro 303
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Db      826 ATGTCAGTGCAGAAAATAACCTGCCTGCTCTTTGTCTGTGGATGCGAGCTGGGAAGTG 885
Qy      304 TrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSer 323
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Db      886 TGGAGTGAATGGTCACTCTGCAGCCAGAGTGTGAACATCTCTCGTATCCGTGAGTGACCA 945
Qy      324 AspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAspThrArgAsn 343
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Db      946 GCTCCACCCCAAGAAATGGGGCAAGTTCTGTGAAGGTCTCAGCAGGAAATCTGAAAC 1005
Qy      344 CysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyrVal 363
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Qy      364 GlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIleLeuValTyr 383
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Qy      384 CysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSerGly 403
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Db      1123 AGACGGAGCCACAGTCACTACGGAGTGGATGTCATTCATTCCTCTCTGCATTCACAGGTGC 1182
Qy      404 PheGlnProValSerIleLysProSerLysAlaAlaAspAsnProHisIleLeuLeu----Thr 421
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Db      1243 ATGCAGCCAGATCTG---ACTGTGAGCCGAGACATACAGCGGCCCATCTCTGT---CTGCAG 1296
Qy      442 AspGlyProSerProLysPheGlnLeuThrAsnGlyHisIleLeuLeuSerProLeuGly--- 460
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Db 1354 ATCAAGTCAAGTCCAGAGCTCATTATGTTTCCCTGGGAGTGTCTGACAGAGCGGAG 1413
Qy 461 -----GlyArgHis-----Thr 465
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Qy 466 LeuHisHisSerSerProThrSerGluAlaGluGluPheValSerArgLeuSerThrGln 485
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Db 1516 -----TACTGCCACAGGACAGAGCTGAGGACACTGGTGTCTTTGGCCAT 1563
Qy 506 LeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProProAspAla 525
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Qy 586 SerTrpSerLeuArgLeuLysGlnSerCysGluGlySerTrpGluAspValLeuHis 605
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Qy 606 LeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSerAlaCysTyr 625
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Qy 766 ValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLysAsp 785
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DEFINITION genomic survey sequence.
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VERSION AY401469.1 GI:39757458
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2775)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2775)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity: 44.73% Mismatches: 302
Query Match: 43.92% Indels: 51
DB: 9 Gaps: 11
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Qy 757 ThrSerAspLeuAlaCysLysLeuTyrValTrpGlnValGluGlyAspGlyGlnSerPhe 776
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RESULT 10
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DEFINITION Pan troglodytes HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY411748
VERSION AY411748.1 GI:39767716
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 2532)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
JOURNAL PUBLISHED
2 (bases 1 to 2532)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
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ORIGIN

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Query Match: 40.02% Indels: 53
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US-10-624-932C-2 (1-898) x AY411748 (1-2532)

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Qy 139 LysAlaTyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLys 158
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Qy 219 TyrThrCysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIle 238
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Qy 239 ValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCys 258
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QY 404 PheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu-----Thr 421
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BC033727
VERSION
BC033727.1
KEYWORDS
HTC
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1532)
AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Maman, A., Rodriguez, S.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzyzinski, M.I., Skalek, U., Smalios, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 2 (bases 1 to 1532)
 Strausberg, R.
 Direct Submission
 Submitted (02-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-re@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayèle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,
 Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
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 Clone distribution: MGC clone distribution information can be found
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KEYWORDS GSS.
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ORGANISM Pan troglodytes
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AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE    Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2507)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE    Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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them based on alignment.
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US-10-624-932C-2 (1-898) x AY401470 (1-2507)

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DB	2	GAGGCGCCCTCCCACTTACTACTGCCAGCTGGAGCCAGTGCCTGCTACGTTTCACC	61	
QY	629	GLUGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAlaLysArg	648	
DB	62	GAGCAGCTGGCGCGCTTGGCTCGTGGAGAGCGCCCTCAGCGTGGCTGGCGCAAGCGC	121	
QY	649	LeuLysLeuLeuLeuPheAlaProValAlaCysThrSerLeuGluTyrAsnIleArgVal	668	
DB	122	CTCAAGCTGCTTCTGTGTGGCGGGTGGCTGCACCTCCCTCGAGTACAAACATCCGGGTC	181	
QY	669	TyrCysLeuHisAspThrHisAspAlaLeuLysGluValValGlnLeuGluLysGlnLeu	688	
DB	182	TACTGCTGATGACACCCACGATGCACCTCAAGAGGTGGTGCAGCTGGAGAGCAGCTG	241	
QY	689	GlyGlyGlnLeuLeuGlnGluProArgValLeuHisPheLysAspSerTyrHisAsnLeu	708	
DB	242	GGGGGACAGCTGATCCAGGAGCCACCGGCTCTGCACCTTCAAGGACAGTTACCAACCTG	301	
QY	709	ArgLeuSerIleHisAspValProSerSerLeuTyrLysSerLysLeuValSerTyr	728	
DB	302	CGCTATCCATCCACGATGCCCCAGCTCCCTGTGAAGAGTAAGCTCTTTGTCAGCTAC	361	
QY	729	GlnGluLeuProPheTyrHisIleTyrAsnGlyThrGlnArgTyrLeuHisCysThrPhe	748	
DB	362	CAGGAGATCCCTTTATCATCTCGAATGGACGCGGGTACTTGCACCTGCACCTTC	421	
QY	749	ThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLeuTyrValTyrGln	768	
DB	422	ACCCTGGAGCGTGTCAAGCCCGACAGCTAGTGCCTGCGCTGCAGCTGTGGGTGGCAG	481	
QY	769	ValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLysAspThrArgPhe	788	
DB	482	GTGGAGGCGGACGGGACAGCTTCAGATCACTTCAACATCACCAAGGACACAAAGTTT	541	
QY	789	AlaGluLeuLeuAlaLeuGluSerGluAlaGlyValProAlaLeuValGlyProSerAla	808	
DB	542	GCTGAGCTGTGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGCCCCAGTGCC	601	
QY	809	PheLysIleProPheLeuIleArgGlnLysIleIleSerSerLeuAspProProCysArg	828	
DB	602	TTCAAGATCCCTTCCTCATTCGGCAGAGATAATTTCCAGCCTGGACCCACCCCTGTAGG	661	
QY	829	ArgGlyValaAspTyrArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPhe	848	
DB	662	CGGGGTGCCACTCGGGGACTCTGGCCAGAACTCCACTCGACAGCCATCTCAGCTTC	721	
QY	849	PheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTyrGluAlaArgHisPhe	868	
DB	722	TTTGCCTCCAAAGCCCGAGCCCAAGCCATGATCTCAACCTGTGGGAGGCGGCGCACTTC	781	
QY	869	ProAsnGlyAsnLeuSerGlnLeuAlaAlaAlaValAlaGlyLeuGlyGlnProAspAla	888	
DB	782	CCCAAGCGCAACCTCAGCCAGCTGGCTGCACAGTGGCTGAGTGGCTGAGTGGCGCAGCGCT	841	
QY	889	GlyLeuPheThrValSerGluAlaGluCys	898	
DB	842	GGCCTCTTACAGTGTGGAGGCTGAGTGC	871	
RESULT 14				
BI758231				
LOCUS				
		1034 bp	mRNA	linear EST 25-SEP-2001

DEFINITION 603029876F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5200171 5', mRNA sequence.

ACCESSION BI758231

VERSION BI758231.1 GI:15749809

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1034)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11501 row: 9 column: 20
High quality sequence stop: 793.
Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.:	1.85e-114	Length:	1034
Score:	1402.00	Matches:	296
Percent Similarity:	89.68%	Conservative:	8
Best Local Similarity:	89.32%	Mismatches:	26
Query Match:	29.26%	Indels:	13
DB:	4	Gaps:	2

US-10-624-932C-2 (1-898) x BI758231 (1-1034)

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QY	56	ValLysAsnLysProValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePhe	75
DB	62	GTCAAGAACCAAGCAGTGTGCTGTGTGCAAGCGGTGCCCGCCACGCAATCTTCTTC	121
QY	76	LysCysAsnGlyGluTyrValArgGlnValAspHisValIleGluArgSerThrAspGly	95
DB	122	AAATGCAACGGGGAGTGGGTGGCCAGGTGGACCCACGTATCGAGCGCAGCAGACGGG	181
QY	96	SerSerGlyLeuProThrMetGluValArgIleAsnValSerArgGlnGlnValGluLys	115
DB	182	AGCAGTGGGCTGCCCAACCATGGAGGTCCGCAATTAATGTCTCAAGCGCAGCGTTCGAGAAG	241
QY	116	ValPheGlyLeuGluGluTyrTrpCysGlnCysValAlaThrSerSerSerGlyThrThr	135
DB	242	GTGTTCCGGCTGGAGGATACTGGTCCAGTGTGGCATGGAGTCTCTGGCGCACACC	301

Qy 136 LysSerGlnLysAlaTyrIleArgIleAlaArgLeuArgLysAsnPhleGluGlnPro 155
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 Qy 156 LeuAlaLysGluValSerLeuGlnGlyIleValLeuProCysArgProProGluGly 175
 Db 362 CTGGCCCAAGAGGTTCTCCCTGGACAGCGCATCTGCTCCCTCCGCTCCACCGAGGCG 421
 Qy 176 IleProAlaGluValGluTyrLeuArgAsnGluAspLeuValAspProSerLeuAsp 195
 Db 422 ATCCCTCCAGCGAGGTGGAGTGGCTCCGGACAGAGACCTGGTGGACCCCTCCCTGGAC 481
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 Db 602 GCTGTCTATCTCTACGTGACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGC 661
 Qy 255 rAlaSerCysGlyArgGlyTyrGlnLys-ArgSerArgSerCysThrAsnProAlaProL 275
 Db 662 -GCCAGCTGTGGCGCGCTGGCAGAAACCGAGCGGAGCTGCAC-AACCGGTGCTC 719
 Qy 275 euAsnGlyGlyAlaPhaCysGlu-GlyGlnAsnValGlnLysThrAlaCysAlaThrLeu 294
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 Qy 295 CysProValAspGlySerTyrSerProTyrSerLysTyrSerAlaCys--GlyLeuAspC 314
 Db 777 GTGCCAGTGACGGCAGCTGTAGCAGCTGGAGCGAGTGGTGGTGGTGGTGGTGGTGGCT 836
 Qy 314 YsThrHis-TripArgSerArgGluCysSerAsp-ProAlaProArgAsnGlyGlyGlu 333
 Db 837 GCACCACTTTGGCGGAGCGGAGTGTCTGACCCAGCAGCCCGGACCGGAGGGGAG 896
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RESULT 15
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 ACCESSION BI818609
 VERSION BI818609.1 GI:15929902
 KEYWORDS EST.
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 818)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-x@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov

Plate: L1AM11434 row: 1 column: 16
 High quality sequence stop: 744.

FEATURES

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 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 Kb,
 insert size range 1-3 Kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 7,01e-110 Length: 818
 Score: 1349.00 Matches: 264
 Percent Similarity: 81.16% Conservative: 3
 Best Local Similarity: 80.24% Mismatches: 4
 Query Match: 28.16% Indels: 58
 DB: 4 Gaps: 1

US-10-624-932C-2 (1-898) x BI818609 (1-818)

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 Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
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 Db 124 GACCTGCTTCCCCACTTCTCTGTGGAGCCGAGGATGTGTACATCGTCAAGACCAAGCCA 183
 Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
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 Qy 121 GluTyrTrpCysGlnCysValAlaIleTyrSerSerSerGlyThrThrLysSerGlnLysAla 140
 Db 364 GAATACTGTGGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 423
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